

SEQUENCE LISTING

<110> Genentech, Inc.
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Stewart, Timothy A.
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<120> Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

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Gln Gly Asp Gly Ser Cys Arg His Met Gly Tyr Gln Gly Pro Leu
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Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
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His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
 195 200 205

Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
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Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
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Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
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Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
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Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys
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Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro
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35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
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Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly			
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Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr			
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Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys			
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195		200	205
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys			
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Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu			
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Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys			
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Glu	Asn	Arg	Gln	Trp	His	Gly	Gly	Ser	Arg	His	Asp	Gln	Ser	His	Gln
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DNA Sequence Database

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 65 70 75 80
 Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
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 Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
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 Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
 115 120 125
 Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
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 Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
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oligonucleotide probe

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44

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<212> DNA

<213> Homo sapiens

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<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

DRAFT - DO NOT CITE

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Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
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Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
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His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr
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<210> 24

<211> 28

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<213> Artificial Sequence

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oligonucleotide probe

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28

<210> 25

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<212> DNA
<213> Homo sapiens

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<211> 660

<212> PRT

<213> Homo sapiens

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				20				25				30			

Leu	Leu	Ala	Cys	Pro	Ser	Val	Cys	Arg	Cys	Asp	Arg	Asn	Phe	Val	Tyr
				35			40				45				

Cys	Asn	Glu	Arg	Ser	Leu	Thr	Ser	Val	Pro	Leu	Gly	Ile	Pro	Glu	Gly
				50			55			60					

Val	Thr	Val	Leu	Tyr	Leu	His	Asn	Asn	Gln	Ile	Asn	Asn	Ala	Gly	Phe
65					70				75				80		

Pro	Ala	Glu	Leu	His	Asn	Val	Gln	Ser	Val	His	Thr	Val	Tyr	Leu	Tyr
					85				90			95			

Gly	Asn	Gln	Leu	Asp	Glu	Phe	Pro	Met	Asn	Leu	Pro	Lys	Asn	Val	Arg
					100			105			110				

Val	Leu	His	Leu	Gln	Glu	Asn	Asn	Ile	Gln	Thr	Ile	Ser	Arg	Ala	Ala
								115		120		125			

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser
 130 135 140

Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser
 145 150 155 160

Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val
 165 170 175

Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile
 180 185 190

Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg
 195 200 205

Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly
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Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn
 225 230 235 240

Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg
 245 250 255

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Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu
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Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln
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Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp
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Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly
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Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro
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Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

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Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met 435	440	445
Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly 450	455	460
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Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu 485	490	495
Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala 500	505	510
Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser 515	520	525
His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala 530	535	540
Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser 545	550	555
Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys 565	570	575
Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly 580	585	590
Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln 595	600	605
Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu 610	615	620
Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His 625	630	635
Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu 645	650	655
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<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

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					20			25							

Ser	Arg	Gly	Arg	His	Ala	Arg	Thr	His	Pro	Gln	Thr	Ala	Leu	Leu	Glu
															45
					35			40							

Ser	Ser	Cys	Glu	Asn	Lys	Arg	Ala	Asp	Leu	Val	Phe	Ile	Ile	Asp	Ser
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					50			55							

Ser	Arg	Ser	Val	Asn	Thr	His	Asp	Tyr	Ala	Lys	Val	Lys	Glu	Phe	Ile
															80
					65		70			75					

Val	Asp	Ile	Leu	Gln	Phe	Leu	Asp	Ile	Gly	Pro	Asp	Val	Thr	Arg	Val
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					85			90							

Gly	Leu	Leu	Gln	Tyr	Gly	Ser	Thr	Val	Lys	Asn	Glu	Phe	Ser	Leu	Lys
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					100			105							

Thr	Phe	Lys	Arg	Lys	Ser	Glu	Val	Glu	Arg	Ala	Val	Lys	Arg	Met	Arg
															125
					115			120							

His	Leu	Ser	Thr	Gly	Thr	Met	Thr	Gly	Leu	Ala	Ile	Gln	Tyr	Ala	Leu
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					130			135							

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Val	Pro	Arg	Val	Ile	Met	Ile	Val	Thr	Asp	Gly	Arg	Pro	Gln	Asp	Ser
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					165			170							

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															190
					180			185							

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Ser	Glu	Pro	His	Glu	Asp	His	Val	Phe	Leu	Val	Ala	Asn	Phe	Ser	Gln
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					210			215							

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Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His			
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Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln			
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Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala			
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Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val			
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Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu			
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Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn			
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Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr			
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Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu			
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Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe			
420	425		430
Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu			
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Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys			
465	470		475
Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu			
485	490		495
His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu			
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Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val
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 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp
 530 535 540
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp
 545 550 555 560
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly
 565 570 575
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys
 580 585 590
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys
 595 600 605
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser
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 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu
 645 650 655
 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn
 660 665 670
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly
 675 680 685
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser
 690 695 700
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg
 705 710 715 720
 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu
 725 730 735
 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly
 740 745 750
 Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro
 755 760 765
 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu
 770 775 780
 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln
 805 810 815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu
 820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp
 835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser
 850 855 860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu
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Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln
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Arg Tyr Arg
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<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 35

gtgaccctgg ttgtgaatac tcc

23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 36

acagccatgg tctatagctt gg

22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 37

gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag

45

<210> 38

<211> 1813

<212> DNA

<213> Homo sapiens

<400> 38

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 gggccatgtat ttccctcccg ggccccctgg tgaccaactt gctcggttt ttgttcctgg 180
 ggctgagtgc cctcgccccc ccctcgccgg cccagctgca actgcacttg cccccaacc 240
 ggttgcaggc ggtggagggg gggaaagtgg tgcttccagc gtggtacacc ttgcacgggg 300
 aggtgtcttc atcccagcca tgggaggtgc cctttgtat gtggttcttc aaacagaaaag 360
 aaaaggagga tcagggtttg tcctacatca atggggtcac aacaagaaa cctggagttat 420
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 tttgtatgaa aaa 1813

<210> 39

<211> 390

<212> PRT

<213> Homo sapiens

<400> 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

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Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln			
20	25	30	
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val			
35	40	45	
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln			
50	55	60	
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys			
65	70	75	80
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro			
85	90	95	
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg			
100	105	110	
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val			
115	120	125	
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr			
130	135	140	
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu			
145	150	155	160
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser			
165	170	175	
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro			
180	185	190	
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser			
195	200	205	
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys			
210	215	220	
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu			
225	230	235	240
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly			
245	250	255	
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His			
260	265	270	
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp			
275	280	285	

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
 290 295 300
 Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg
 305 310 315 320
 Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
 325 330 335
 Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly
 340 345 350
 Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser
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 Gln Ala Gly Ser Leu Val
 385 390
 <210> 40
 <211> 22
 <212> DNA
 <213> Artificial Sequence
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 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe
 <400> 40
 agggtctcca ggagaaagac tc 22
 <210> 41
 <211> 24
 <212> DNA
 <213> Artificial Sequence
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 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe
 <400> 41
 atttgtggcc ttgcagacat agac 24
 <210> 42
 <211> 50
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

ESTIMATE OF THE NUMBER OF NUCLEOTIDES IN THE SEQUENCES

<400> 42		
ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc		50
<210> 43		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 43		
gtgtgacaca gcgtgggc		18
<210> 44		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 44		
gaccggcagg cttctgct		18
<210> 45		
<211> 25		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 45		
cagcagcttc agccaccagg agtgg		25
<210> 46		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 46		
ctgagccgtg ggctgcagtc tcgc		24
<210> 47		

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 47
ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48
<211> 2822
<212> DNA
<213> Homo sapiens

<400> 48
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tcacaatttgc tgaagatgtat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240
ctaattgcac taacacagaa ggaaggattt attgtatgtg tgtacctggc ttcagatcca 300
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caaactgcca ttttagataat gtctgtatag ctgcaaataat taataaaaact ttaacaaaaa 420
tcagatccat aaaagaacct gtggcttgc tacaagaatgt ctatagaaat tctgtgacag 480
atcttcacc aacagatata attacatata tagaaatattt agctgaatca tcttcattac 540
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 acctccacaa attgaa 2820
 aa 2822

<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

Met	Lys	Arg	Leu	Pro	Leu	Leu	Val	Val	Phe	Ser	Thr	Leu	Leu	Asn	Cys
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Ser	Tyr	Thr	Gln	Asn	Cys	Thr	Lys	Thr	Pro	Cys	Leu	Pro	Asn	Ala	Lys
						20		25					30		

Cys	Glu	Ile	Arg	Asn	Gly	Ile	Glu	Ala	Cys	Tyr	Cys	Asn	Met	Gly	Phe
						35		40				45			

Ser	Gly	Asn	Gly	Val	Thr	Ile	Cys	Glu	Asp	Asp	Asn	Glu	Cys	Gly	Asn
	50				55						60				

Leu	Thr	Gln	Ser	Cys	Gly	Glu	Asn	Ala	Asn	Cys	Thr	Asn	Thr	Glu	Gly
	65					70				75			80		

Ser	Tyr	Tyr	Cys	Met	Cys	Val	Pro	Gly	Phe	Arg	Ser	Ser	Ser	Asn	Gln
				85					90				95		

Asp	Arg	Phe	Ile	Thr	Asn	Asp	Gly	Thr	Val	Cys	Ile	Glu	Asn	Val	Asn
					100			105			110				

Ala	Asn	Cys	His	Leu	Asp	Asn	Val	Cys	Ile	Ala	Ala	Asn	Ile	Asn	Lys
						115		120			125				

Thr	Leu	Thr	Lys	Ile	Arg	Ser	Ile	Lys	Glu	Pro	Val	Ala	Leu	Leu	Gln
				130			135				140				

Glu	Val	Tyr	Arg	Asn	Ser	Val	Thr	Asp	Leu	Ser	Pro	Thr	Asp	Ile	Ile
	145				150				155			160			

Thr	Tyr	Ile	Glu	Ile	Leu	Ala	Glu	Ser	Ser	Ser	Leu	Leu	Gly	Tyr	Lys
					165			170			175				

Asn	Asn	Thr	Ile	Ser	Ala	Lys	Asp	Thr	Leu	Ser	Asn	Ser	Thr	Leu	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

180	185	190
Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val		
195	200	205
Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys		
210	215	220
Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe		
225	230	235
Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys		
245	250	255
Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met		
260	265	270
Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala		
275	280	285
Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser		
290	295	300
Ile Gly Pro Leu Leu Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln		
305	310	315
Asn Tyr Asp Asn Ser Glu Glu Glu Arg Val Ile Ser Ser Val Ile		
325	330	335
Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys		
340	345	350
Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser		
355	360	365
Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp		
370	375	380
Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser		
385	390	395
Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly		
405	410	415
Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln		
420	425	430
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr		
435	440	445
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys		
450	455	460

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
 465 470 475 480
 Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
 485 490 495
 Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
 500 505 510
 Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
 515 520 525
 Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
 530 535 540
 Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
 545 550 555 560
 Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
 565 570 575
 Pro Ala Cys' Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
 580 585 590
 Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
 595 600 605
 Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
 610 615 620
 Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
 625 630 635 640
 Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
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 Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
 660 665 670
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 675 680 685
 Leu Arg
 690
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 <212> DNA
 <213> Homo sapiens
 <220>
 <221> modified_base
 <222> (61)

<223> a, t, c or g

<400> 50

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 ngaaaagccg gcatatggat tcaaattggca atgttgcagt tgcatttttta tattataaga 120
 gtattggtcc ctttgcttcc atcatctgac aacttcttat tgaaacacctca aaattatgat 180
 aattctgaag aggagggaaag agtcataatct tcagtaattt cagtcataat gagctcaaac 240
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 gataggtata ggagtctatg tgcattttg gaatactcac ctgataccat gaatggcagc 360
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<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg

18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 54
cgagctcgaa ttaattcg 18

<210> 55
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 55
ggatctcctg agtcagg 18

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 56
cctagttgag tgatccttgt aag 23

<210> 57
<211> 50
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 57
atgagaccca cacctcatgc cgctgtataac acctgacaca ttttgcaatt 50

<210> 58
<211> 2137
<212> DNA
<213> Homo sapiens

<400> 58
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<210> 59
<211> 216
<212> PRT
<213> *Homo sapiens*

<400> 59
Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
1 5 10 15

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
65 70 75 80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
 180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
195 200 205

Val Arg Ser Pro Ser Phe Glu Lys
210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 60

atccggcccaag atggctacaa tgtgtta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 61

gcctcccggt ctccctgagc agtgccaaac agcggcagtg ta

42

<210> 62
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 62
 ccagtccggc gacaagcccc aa 22

<210> 63
 <211> 1295
 <212> DNA
 <213> Homo sapiens

<400> 63
 cccagaagtt caagggcccc cggcctcctg cgctcctgcc gccgggaccc tcgacccct 60
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 gctgtctg cgctacctgg tggctccct gggctatcat aaggcctatg gttttctgc 180
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggctattt tagcctgcaa 240
 aaccccaaag aagactgttt cctccagatt agagtggaaag aaactgggtc ggagtgtctc 300
 ctttgtctac tatcaacaga ctcttcagg tgatttaaa atcggatctg agatgataga 360
 tttcaatatac cggatcaaaa atgtgacaag aagtgtatgc gggaaatatac gttgtgaagt 420
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<210> 64
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 64
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 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
 35 40 45

Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
 50 55 60

Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
 65 70 75 80

Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
 85 90 95

Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
 100 105 110

Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
 115 120 125

Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
 130 135 140

Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
 145 150 155 160

Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
 165 170 175

Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met
 180 185 190

Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp
 195 200 205

Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg
 210 215 220

Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile
 225 230 235 240

Ile Ala Ala Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu
 245 250 255

Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser
 260 265 270

Phe Gln Lys Ser Asn Ser Ser Lys Ala Thr Thr Met Ser Glu Asn
 275 280 285

Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala
 290 295 300

Gly Gly Ser Arg Gly Gln Glu Phe

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<pre> <220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe </pre>		
<pre> <400> 65 atcgttgtga agttagtgcc cc </pre>		
<pre> <210> 66 <211> 23 <212> DNA <213> Artificial Sequence </pre>		
<pre> <220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe </pre>		
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<pre> <210> 67 <211> 48 <212> DNA <213> Artificial Sequence </pre>		
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<pre> <210> 68 <211> 2639 <212> DNA <213> Homo sapiens </pre>		
<pre> <400> 68 gacatcgagg gtgggctagc actgaaaactg cttttcaaga cgaggaagag gaggagaaag 60 agaaaagaaga ggaagatgtt gggcaacatt tatttaacat gctccacagc ccggaccctg 120 gcatcatgct gctattccctg caaatactga agaagcatgg gatttaaata ttttacttct 180 aaataaaatga attactcaat ctcctatgac catctataca tactccacct tcaaaaagta 240 catcaaatatt atatcattaa gggaaatagta accttctctt ctccaaatatg catgacattt 300 ttggacaatg caattgtggc actggcactt atttcagtga agaaaaaactt tgtggttcta 360 tggcattcat catttgacaa atgcaagcat cttccttatac aatcagctcc tattgaactt 420 actagcactg actgtgaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480 tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagta 540 </pre>		

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<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

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Cys	Thr	Cys	Glu	Ile	Arg	Pro	Trp	Phe	Thr	Pro	Arg	Ser	Ile	Tyr	Met
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Glu	Ala	Ser	Thr	Val	Asp	Cys	Asn	Asp	Leu	Gly	Leu	Leu	Thr	Phe	Pro
				50			55					60			

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn
 65 70 75 80

Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly
 85 90 95

Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val
 100 105 110

Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu
 115 120 125

Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu
 130 135 140

Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe
 145 150 155 160

Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu
 165 170 175

Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile
 180 185 190

Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe
 195 200 205

Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu
 210 215 220

Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser
 225 230 235 240

Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu
 245 250 255

Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile
 260 265 270

Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu
 275 280 285

Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala
 290 295 300

Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro
 305 310 315 320

Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu
 325 330 335

Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

340	345	350
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn		
355	360	365
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr		
370	375	380
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro		
385	390	395
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met		
405	410	415
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu		
420	425	430
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala		
435	440	445
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu		
450	455	460
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr		
465	470	475
480		
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys		
485	490	495
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys		
500	505	510
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys		
515	520	525
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser		
530	535	540
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr		
545	550	555
560		
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys		
565	570	575
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys		
580	585	590
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
595	600	605
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
610	615	620

4

Asn	Thr	Thr	Thr	Leu	Met	Ala	Cys	Leu	Gly	Gly	Leu	Leu	Gly	Ile	Ile	
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630 635																
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645 650																
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660 665																
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675 680																
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Thr	Asn	Met	Ser													
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<213>	Homo sapiens															
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Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val			
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Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro			
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Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala			
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Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val			
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His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn			
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Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met			
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165	170	175	
Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala			
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Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val			
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210	215	220	
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<210> 72

<211> 2290

<212> DNA

<213> Homo sapiens

<400> 72

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 aaaaaaaaaa 2290

<210> 73

<211> 620

<212> PRT

<213> Homo sapiens

<400> 73

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Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly
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Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys
 35 40 45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala
 50 55 60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys
 65 70 75 80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His
 85 90 95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro
 100 105 110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser
 115 120 125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn
 130 135 140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp
 145 150 155 160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp
 165 170 175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser
 180 185 190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr
 195 200 205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His
 210 215 220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg
 225 230 235 240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr
 245 250 255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His
 260 265 270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr
 275 280 285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly
 290 295 300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly
 305 310 315 320

Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr
 325 330 335

Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu
 340 345 350

Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser
 355 360 365

Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg
 370 375 380

Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu
 385 390 395 400

Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro
 405 410 415

Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln
 420 425 430

Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala
 435 440 445

Asp Gly Asp Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His
 450 455 460

Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly
 465 470 475 480

Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu
 485 490 495

Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu
 500 505 510

His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr
 515 520 525

Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr
 530 535 540

Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala
 545 550 555 560

Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu
 565 570 575

Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

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<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 78 gggaatagat gtgatctgat tgg	23
<210> 79 <211> 50 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 79 cacctgttagc aatgcaaatac tcaaggaaat acctagagat ctccctcctg	50
<210> 80 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 80 agcaaccgcc tgaagctcat cc	22
<210> 81 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 81 aaggcgccgtt gaaagatgt aacg	24
<210> 82	

<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 82
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<210> 83
 <211> 1685
 <212> DNA
 <213> Homo sapiens

<400> 83
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 agccaggggag cccggccggga agcgcgatgg gggcccccagc cgcctcgctc ctgctccctgc 180
 tcctgctgtt cgcctgctgc tgggcggcccg qcggggccaa cctctcccaag gacgacagcc 240
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 tgaaagatca cgaggactca tccctgcaat ggtctaaccct tgctcagcag actctctact 360
 ttggggagaa gagagccctt cgagataatc gaattcagct gtttacctt acgc当地ccacg 420
 agtcagcat cagcatcagc aatgtggccc tggcagacga gggc当地gatc acctgctcaa 480
 tcttcactat gcctgtgcga actgccaatg ccctcgctac tgtgtctaga attccacaga 540
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 gtgacagtgg cacctacggc tgc当地cagcc ccagcaacat gggc当地gctac aaggc当地act 1080
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 aaaca 1685

<210> 84
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 84

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Cys	Cys	Trp	Ala	Pro	Gly	Gly	Ala	Asn	Leu	Ser	Gln	Asp	Asp	Ser	Gln
					20				25					30	
Pro	Trp	Thr	Ser	Asp	Glu	Thr	Val	Val	Ala	Gly	Gly	Thr	Val	Val	Leu
						35			40				45		
Lys	Cys	Gln	Val	Lys	Asp	His	Glu	Asp	Ser	Ser	Leu	Gln	Trp	Ser	Asn
						50			55				60		
Pro	Ala	Gln	Gln	Thr	Leu	Tyr	Phe	Gly	Glu	Lys	Arg	Ala	Leu	Arg	Asp
					65			70			75			80	
Asn	Arg	Ile	Gln	Leu	Val	Thr	Ser	Thr	Pro	His	Glu	Leu	Ser	Ile	Ser
					85				90					95	
Ile	Ser	Asn	Val	Ala	Leu	Ala	Asp	Glu	Gly	Glu	Tyr	Thr	Cys	Ser	Ile
					100			105				110			
Phe	Thr	Met	Pro	Val	Arg	Thr	Ala	Lys	Ser	Leu	Val	Thr	Val	Leu	Gly
					115			120				125			
Ile	Pro	Gln	Lys	Pro	Ile	Ile	Thr	Gly	Tyr	Lys	Ser	Ser	Leu	Arg	Glu
					130			135			140				
Lys	Asp	Thr	Ala	Thr	Leu	Asn	Cys	Gln	Ser	Ser	Gly	Ser	Lys	Pro	Ala
					145			150			155			160	
Ala	Arg	Leu	Thr	Trp	Arg	Lys	Gly	Asp	Gln	Glu	Leu	His	Gly	Glu	Pro
					165				170				175		
Thr	Arg	Ile	Gln	Glu	Asp	Pro	Asn	Gly	Lys	Thr	Phe	Thr	Val	Ser	Ser
					180			185				190			
Ser	Val	Thr	Phe	Gln	Val	Thr	Arg	Glu	Asp	Asp	Gly	Ala	Ser	Ile	Val
					195			200				205			
Cys	Ser	Val	Asn	His	Glu	Ser	Leu	Lys	Gly	Ala	Asp	Arg	Ser	Thr	Ser
					210			215			220				
Gln	Arg	Ile	Glu	Val	Leu	Tyr	Thr	Pro	Thr	Ala	Met	Ile	Arg	Pro	Asp
					225			230			235			240	
Pro	Pro	His	Pro	Arg	Glu	Gly	Gln	Lys	Leu	Leu	Leu	His	Cys	Glu	Gly
					245			250				255			
Arg	Gly	Asn	Pro	Val	Pro	Gln	Gln	Tyr	Leu	Trp	Glu	Lys	Glu	Gly	Ser
					260			265				270			
Val	Pro	Pro	Leu	Lys	Met	Thr	Gln	Glu	Ser	Ala	Leu	Ile	Phe	Pro	Phe
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Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser
 305 310 315 320

Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
 385 390 395

<210> 85
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 85
 gcttaggaatt ccacagaagc cc 22

<210> 86
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 86
 aaccttggaaat gtcaccgagc tg 22

<210> 87
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 87		
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<210> 88		
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<212> DNA		
<213> Artificial Sequence		
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<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 88		
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<210> 89		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
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<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
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gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt		50
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<212> DNA		
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<210> 91
 <211> 696
 <212> PRT
 <213> Homo sapiens

<400> 91																	
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														30			
Glu	Ile	Glu	Gly	Asp	Leu	His	Val	Asp	Cys	Glu	Lys	Lys	Gly	Phe	Thr		
														45			
Ser	Leu	Gln	Arg	Phe	Thr	Ala	Pro	Thr	Ser	Gln	Phe	Tyr	His	Leu	Phe		
														50	55	60	
Leu	His	Gly	Asn	Ser	Leu	Thr	Arg	Leu	Phe	Pro	Asn	Glu	Phe	Ala	Asn		
														65	70	75	80
Phe	Tyr	Asn	Ala	Val	Ser	Leu	His	Met	Glu	Asn	Asn	Gly	Leu	His	Glu		
														85	90	95	

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His
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 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly
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 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp
 130 135 140
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile
 145 150 155 160
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr
 165 170 175
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu
 180 185 190
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu
 195 200 205
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys
 210 215 220
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val
 225 230 235 240
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr
 245 250 255
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro
 260 265 270
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr
 275 280 285
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala
 290 295 300
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg
 305 310 315 320
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala
 325 330 335
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly
 340 345 350
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala
 355 360 365
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn
 385 390 395 400

Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn
 405 410 415

Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser
 420 425 430

Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn
 435 440 445

Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro
 450 455 460

Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn
 465 470 475 480

Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu
 485 490 495

Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala
 500 505 510

Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly
 515 520 525

Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala
 530 535 540

Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr
 545 550 555 560

Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu
 565 570 575

Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His
 580 585 590

Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser
 595 600 605

Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu
 610 615 620

Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val
 625 630 635 640

Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser
 645 650 655

Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

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Cys Gly Ser His Ser Leu Ser Asp		
690	695	
<210> 92		
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<212> DNA		
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<220>		
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<212> DNA		
<213> Artificial Sequence		
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<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

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Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly
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Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr		
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Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln		
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Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu		
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Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val		
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Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu		
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<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

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35 40 45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
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Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu
 370 375 380

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<210> 105
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<212> DNA
<213> Artificial Sequence

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<210> 106
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<210> 108
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<212> DNA

<213> Homo sapiens

<400> 108

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<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

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Cys	Arg	Gly	Leu	Val	Asp	Ser	Phe	Asn	Lys	Gly	Leu	Glu	Arg	Thr	Ile
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Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr			
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ggacaaatgc tctgtgtct ctgtgagcc ctgaatttgc ttccctgtac aagttacctc 1320
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aaagtccctcc accaccactc tgacctaag acctgggtt aagtgtgggt tgtgcacccc 1560
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<210> 114
 <211> 366
 <212> PRT
 <213> Homo sapiens

<400> 114

Met	Gln	Pro	Leu	Trp	Leu	Cys	Trp	Ala	Leu	Trp	Val	Leu	Pro	Leu	Ala
1															15

Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu
 20 25 30

Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
 35 40 45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
 50 55 60

Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
 65 70 75 80

Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
 85 90 95

His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
 100 105 110

Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
 115 120 125

Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
 130 135 140

Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
 145 150 155 160

Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
 165 170 175

Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
 180 185 190

Pro Arg Gln Pro Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
 195 200 205

Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
 210 215 220

Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
 225 230 235 240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
 245 250 255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
 260 265 270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
 275 280 285

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu
 290 295 300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
 305 310 315 320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
 325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser
 340 345 350

 Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
 355 360 365

 <210> 115
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 115
 aggactgcc a taacttgccct g 21

 <210> 116
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 116
 ataggagttg a a g c a g c g c t g c 22

 <210> 117
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 117
 tgtgtggaca t a g a c g a g t g c c g c t a c c g c tactgcc a c c g c 45

 <210> 118
 <211> 1857
 <212> DNA
 <213> Homo sapiens

 <400> 118
 gtctgttccc aggagtcc tt cggcggttgt t g t g t c a g t g c c g c t g a t c g c g a t g g g g a c a 60
 a a g g c g c a a g t c g a g a g g a a a c t g t t g t g c c t c t t c a t a t t g g c g a t c c t g t g c t c c 120
 c t g g c a t t g g c a g t g t t a c a g t g c a c t c t c t g a a c c t g a a g t c a g a a t t c c t g a g a a t 180

aatcctgtga agtgtgcctg tgcctactcg ggcttttctt ctccccgtgt ggagtggaa 240
tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300
gaggaccggg tgacccctt gccaactggt atcacctca agtccgtgac acgggaagac 360
actgggacat acaattgtat ggtctcgtag gaaggcggca acagctatgg ggaggtcaag 420
gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctcctctgcc 480
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tacaccttgt tcaaagatgg gatagtgtat cctacgaatc caaaaagcac cegtgccctc 600
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ggagaaaaccc tactggaaat acaaagttag ccaggcatgg tgggttcacg ctgttagtccc 1800
agctgctcag ggcctggca acaagagcaa aactccagct caaaaaaaaaaa aaaaaaaaaa 1857

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

Met Gly Th

1 **5** **10** **15**

20 25 30

10

35 40 45

3

4

-

50 55 60

50

53

60

Asp. City Asp. Inn. Inn. Reg. Reg. Reg. Val. 65 70 75 80

65

70

75

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
85 90 95

85

90

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
 100 105 110
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
 115 120 125
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
 130 135 140
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
 145 150 155 160
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
 165 170 175
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
 180 185 190
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
 195 200 205
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
 210 215 220
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
 225 230 235 240
 Ala Ala Val Leu Val Thr Leu Ile Leu Gly Ile Leu Val Phe Gly
 245 250 255
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
 260 265 270
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
 275 280 285
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
 290 295
 <210> 120
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe
 <400> 120
 tcgcggagct gtgttctgtt tccc
 <210> 121
 <211> 50

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 121
tgatcgcgat ggggacaaag gcgcaggctc gagaggaaac tgttgtgcct 50

<210> 122
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 122
acacacctgggtt caaagatggg 20

<210> 123
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 123
taggaagagt tgctgaaggc acgg 24

<210> 124
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 124
ttgccttact caggtgctac 20

<210> 125
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
 85 90 95

 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
 100 105 110

 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
 115 120 125

 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
 130 135 140

 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
 145 150 155 160

 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
 165 170 175

 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
 180 185 190

 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
 195 200 205

 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
 210 215 220

 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala
 225 230 235 240

 Ser Leu Val Thr Ala Thr Leu Leu Leu Ser Trp Leu Arg Ala Gln
 245 250 255

 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
 260 265 270

 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
 275 280

 <210> 128
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 128
 aagttccagt gccgcaccag tggc

 <210> 129

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 129
 ttggttccac agccgagctc gtcg 24

<210> 130
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 130
 gaggaggagt gcaggattga gccatgtacc cagaaaggc aatgccacc 50

<210> 131
 <211> 1843
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1837)
 <223> a, t, c or g

<400> 131
 cccacgcgtc cggctctcgct cgctcgcgca gcggcgccag cagaggtcgc gcacagatgc 60
 gggttagact ggccccggga ggaggcgag gagggaaagga agctgcataatgc atgagaccca 120
 cagactcttg caagctggat gcccctgtg gatgaaaatgtatcatgaa atgaacccga 180
 gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
 gactcttggc cgtgatcctg tggtttcagc tggcgctgtg ctccggccct gcacagctca 300
 cggcggggtt cgatgaccctt caagtgtgtg ctgacccccgg cattccccgag aatggcttca 360
 ggaccccccag cggagggggtt ttctttgaag gctctgttagc ccgatttcac tgccaaagacg 420
 gattcaagct gaaggccgct acaaagagac tgtgtttgaa gcattttaat ggaaccttag 480
 gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgcccgtatc cctcaaatcg 540
 aagatgtga gattcataac aagacatata gacatggaga gaagctaatc atcacttgtc 600
 atgaaggatt caagatccgg taccccgacc tacacaatat gtttcatat tgtcgccatg 660
 atgaaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctttctta 720
 atggctatgt aaacatctct gagctccaga cctccctccc ggtggggact gtgatctct 780
 atcgctgctt tcccgattt aaacttgatg ggtctcgta tcttgatgtc ttacaaaacc 840
 ttatctggtc gtccagccca cccccgggtcc ttgctctggaa agcccaagtc tgtccactac 900
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cgccaaccag tgtgctgctg gtgctgctgc tcgtcatcct gcccaggatg ttccagacca 1200
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 cggcagagga ggtggcatcc accagcccg gcatccatca tgcccactgg gtgtgttcc 1620
 taagaaaactg attgataaaa aaatttccca aagtgcctg aagtgtctct tcaaatacat 1680
 gttgatctgt ggagttgatt ccttgccttc tcttggttt agacaaatgt aaacaaagct 1740
 ctgatcctta aaattgctat gctgatagag tggtgaggc tggaaagctt atcaagtcc 1800
 gttcttctt gacacagact gattaataaa taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met	Tyr	His	Gly	Met	Asn	Pro	Ser	Asn	Gly	Asp	Gly	Phe	Leu	Glu	Gln
1				5				10						15	

Gln	Gln	Gln	Gln	Gln	Pro	Gln	Ser	Pro	Gln	Arg	Leu	Leu	Ala	Val
					20			25					30	

Ile	Leu	Trp	Phe	Gln	Leu	Ala	Leu	Cys	Phe	Gly	Pro	Ala	Gln	Leu	Thr
				35				40					45		

Gly	Gly	Phe	Asp	Asp	Leu	Gln	Val	Cys	Ala	Asp	Pro	Gly	Ile	Pro	Glu
				50				55					60		

Asn	Gly	Phe	Arg	Thr	Pro	Ser	Gly	Gly	Val	Phe	Phe	Glu	Gly	Ser	Val
65					70				75					80	

Ala	Arg	Phe	His	Cys	Gln	Asp	Gly	Phe	Lys	Leu	Lys	Gly	Ala	Thr	Lys
					85				90					95	

Arg	Leu	Cys	Leu	Lys	His	Phe	Asn	Gly	Thr	Leu	Gly	Trp	Ile	Pro	Ser
					100				105				110		

Asp	Asn	Ser	Ile	Cys	Val	Gln	Glu	Asp	Cys	Arg	Ile	Pro	Gln	Ile	Glu
				115				120					125		

Asp	Ala	Glu	Ile	His	Asn	Lys	Thr	Tyr	Arg	His	Gly	Glu	Lys	Leu	Ile
					130			135					140		

Ile	Thr	Cys	His	Glu	Gly	Phe	Lys	Ile	Arg	Tyr	Pro	Asp	Leu	His	Asn
							145		150				155		160

Met	Val	Ser	Leu	Cys	Arg	Asp	Asp	Gly	Thr	Trp	Asn	Asn	Leu	Pro	Ile
					165				170				175		

Cys	Gln	Gly	Cys	Leu	Arg	Pro	Leu	Ala	Ser	Ser	Asn	Gly	Tyr	Val	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

180	185	190
Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr		
195	200	205
Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys		
210	215	220
Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu		
225	230	235
Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe		
245	250	255
Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val		
260	265	270
Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr		
275	280	285
Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys		
290	295	300
Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr		
305	310	315
Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu		
325	330	335
Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His		
340	345	350
Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe		
355	360	365
Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala		
370	375	380
Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val		
385	390	395
Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr		
405	410	415
Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys		
420	425	430
Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro		
435	440	445
Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile		
450	455	460

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn
 485 490

<210> 133
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 133
atccctatc gctgcttcc cg 23

<210> 134
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 134
agccaggatc gcagtaaaac tcc 23

<210> 135
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 135
atttaaactt gatgggtctg cgtatcttga gtgcttacaa aactttatct 50

<210> 136
<211> 1815
<212> DNA
<213> Homo sapiens

<400> 136
cccacgcgtc cgctccgcgc cctccccccc gcctcccggtg cggccgtcg gtggccataga 60
gatgctgctg ccgcgggtgc agttgtcgcg cacgcctctg cccgcgcaccc cgctccaccg 120
ccgtagegcc cgagtgtcggtt ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180
tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcacgc ggtcgccctgc 240
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 ggccagacact gaagaatatt tcattccgag tgggttcggg agaagccact cccgatgaca 1140
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 agcaggaaaa aaaaaa 1815

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met	Arg	Pro	Gly	Thr	Ala	Leu	Gln	Ala	Val	Leu	Leu	Ala	Val	Leu	Leu
1					5				10				15		

Val	Gly	Leu	Arg	Ala	Ala	Thr	Gly	Arg	Leu	Leu	Ser	Ala	Ser	Asp	Leu
					20				25				30		

Asp	Leu	Arg	Gly	Gly	Gln	Pro	Val	Cys	Arg	Gly	Gly	Thr	Gln	Arg	Pro
					35			40				45			

Cys	Tyr	Lys	Val	Ile	Tyr	Phe	His	Asp	Thr	Ser	Arg	Arg	Leu	Asn	Phe
					50			55				60			

Glu	Glu	Ala	Lys	Glu	Ala	Cys	Arg	Arg	Asp	Gly	Gly	Gln	Leu	Val	Ser
					65			70			75		80		

Ile	Glu	Ser	Glu	Asp	Glu	Gln	Lys	Leu	Ile	Glu	Lys	Phe	Ile	Glu	Asn
					85			90				95			

Leu	Leu	Pro	Ser	Asp	Gly	Asp	Phe	Trp	Ile	Gly	Leu	Arg	Arg	Glu	
					100			105				110			

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
 115 120 125
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
 130 135 140
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
 145 150 155 160
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
 165 170 175
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
 180 185 190
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
 195 200 205
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
 210 215 220
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
 225 230 235 240
 Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
 245 250 255
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
 260 265 270
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
 275 280 285
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
 290 295 300
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly
 305 310 315 320
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val
 325 330 335
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
 340 345 350
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg
 355 360 365
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr
 370 375 380

<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 138
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 139
 aagccaaaga agcctgcagg aggg 24

<210> 140
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 140
 cagtccaagc ataaagggtcc tggc 24

<210> 141
 <211> 1514
 <212> DNA
 <213> Homo sapiens

<400> 141
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<210> 142
 <211> 428
 <212> PRT
 <213> Homo sapiens

<400> 142
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 20 25 30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
 35 40 45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
 50 55 60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
 65 70 75 80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
 85 90 95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
 100 105 110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
 115 120 125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
 130 135 140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
 145 150 155 160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
 165 170 175

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His
 180 185 190

 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys
 195 200 205

 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu
 210 215 220

 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly
 225 230 240

 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val
 245 250 255

 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg
 260 265 270

 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile
 275 280 285

 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe
 290 295 300

 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr
 305 310 320

 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val
 325 330 335

 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp
 340 345 350

 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu
 355 360 365

 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val
 370 375 380

 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn
 385 390 400

 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys
 405 410 415

 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
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<210> 143
 <211> 24
 <212> DNA
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 143
      ccaactacca aagctgctgg agcc                                24

<210> 144
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 144
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<210> 145
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 145
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<210> 146
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 146
      ggcagagaac cagaggccgg aggagactgc ctcttacag ccagg      45

<210> 147
<211> 1686
<212> DNA
<213> Homo sapiens

<400> 147
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      ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctgggtggg 180

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<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

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Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
 35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
 50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Glu Gln Glu Val Tyr
 100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
 115 120 125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
 130 135 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
 145 150 155 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
 165 170 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
 180 185 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
 195 200 205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
 210 215 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
 225 230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
 245 250 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
 260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
 275 280 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
 290 295 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
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Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
 325 330 335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val
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<210> 149
 <211> 24
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

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<210> 150		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 150		
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<210> 151		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
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gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt		50
<210> 152		
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<212> DNA		
<213> Homo sapiens		
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<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

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															30
20															

Ala	Tyr	Leu	Arg	Asn	Ala	Val	Val	Val	Ile	Thr	Gly	Ala	Thr	Ser	Gly
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35															

Leu	Gly	Lys	Glu	Cys	Ala	Lys	Val	Phe	Tyr	Ala	Ala	Gly	Ala	Lys	Leu
															60
50															

Val	Leu	Cys	Gly	Arg	Asn	Gly	Gly	Ala	Leu	Glu	Glu	Leu	Ile	Arg	Glu
															80
65															

Leu	Thr	Ala	Ser	His	Ala	Thr	Lys	Val	Gln	Thr	His	Lys	Pro	Tyr	Leu
															95
85															

Val	Thr	Phe	Asp	Leu	Thr	Asp	Ser	Gly	Ala	Ile	Val	Ala	Ala	Ala	Ala
															110
100															

Glu	Ile	Leu	Gln	Cys	Phe	Gly	Tyr	Val	Asp	Ile	Leu	Val	Asn	Asn	Ala
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115															

Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Ile	Met	Asp	Thr	Thr	Val	Asp	Val	Asp
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130															

Lys	Arg	Val	Met	Glu	Thr	Asn	Tyr	Phe	Gly	Pro	Val	Ala	Leu	Thr	Lys
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145															

Ala	Leu	Leu	Pro	Ser	Met	Ile	Lys	Arg	Arg	Gln	Gly	His	Ile	Val	Ala
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165															

Ile	Ser	Ser	Ile	Gln	Gly	Lys	Met	Ser	Ile	Pro	Phe	Arg	Ser	Ala	Tyr
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Ala	Ala	Ser	Lys	His	Ala	Thr	Gln	Ala	Phe	Phe	Asp	Cys	Leu	Arg	Ala
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195															

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210	215	220
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225	230	235
Tyr Gly Val Met Asp Thr Thr Ala Gln Gly Arg Ser Pro Val Glu		
245	250	255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Asp Val		
260	265	270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu		
275	280	285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu		
290	295	300
Arg Lys Ser Lys Asn Ser		
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<210> 154		
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<220>		
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oligonucleotide probe		
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<212> DNA		
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oligonucleotide probe		

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<210> 158		
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<213> Homo sapiens		
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<211> 300

<212> PRT

<213> Homo sapiens

<400> 159

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Cys	Ser	Leu	Glu	Ser	Phe	Val	Lys	Leu	Phe	Ile	Pro	Lys	Arg	Arg	Lys
						20		25				30			

Ser	Val	Thr	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	His	Gly	Ile
						35		40			45				

Gly	Arg	Leu	Thr	Ala	Tyr	Glu	Phe	Ala	Lys	Leu	Lys	Ser	Lys	Leu	Val
						50		55		60					

Leu	Trp	Asp	Ile	Asn	Lys	His	Gly	Leu	Glu	Glu	Thr	Ala	Ala	Lys	Cys
						65		70		75		80			

Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe	Val	Val	Asp	Cys	Ser	Asn
						85		90			95				

Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys	Lys	Val	Lys	Ala	Glu	Ile	Gly
						100		105			110				

Asp	Val	Ser	Ile	Leu	Val	Asn	Asn	Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp
						115		120			125				

Leu	Phe	Ala	Thr	Gln	Asp	Pro	Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn
						130		135		140					

Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr
						145		150		155		160			

Lys	Asn	Asn	His	Gly	His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His
						165		170		175					

Val	Ser	Val	Pro	Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala
						180		185			190				

Val	Gly	Phe	His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Leu	Gln	Ile
						195		200			205				

Thr	Gly	Val	Lys	Thr	Thr	Cys	Leu	Cys	Pro	Asn	Phe	Val	Asn	Thr	Gly
						210		215		220					

Phe	Ile	Lys	Asn	Pro	Ser	Thr	Ser	Leu	Gly	Pro	Thr	Leu	Glu	Pro	Glu
						225		230		235		240			

Glu	Val	Val	Asn	Arg	Leu	Met	His	Gly	Ile	Leu	Thr	Glu	Gln	Lys	Met
						245		250			255				

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile
 260 265 270
 Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys
 275 280 285
 Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
 290 295 300

<210> 160
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 160
 ggtgaaggca gaaattggag atg 23

<210> 161
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 161
 atccccatgca tcagcctgtt tacc 24

<210> 162
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 162
 gctggtag tctatacatc agattttttt gctacacaag atcctcag 48

<210> 163
 <211> 2076
 <212> DNA
 <213> Homo sapiens

<400> 163
 cccacgcgtc cgccggacgcg tggttcgact agttcttagat cgccgagcgcc cgcccgccgc 60
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tttgggggg agatgttac tacaaaatta acatgagtagt atgagaaga attacattat 1740
ttaactaaa ggtgaaagg tatggatgt gtgacactga gacaagatgt ataaatgaaa 1800
ttttagggc ttgaatagga agtttaatt tcttctaaga gtaagtgaaa agtgcagttg 1860
taacaaacaa agctgtaaaca tcttttctg ccaataacag aagttggca tgccgtgaag 1920
gtgttgaa atattattgg ataagaatag ctcaattatc ccaaataaat ggatgaagct 1980
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qaaataaaaa tattatatat aaaactaaaa aaaaaaa 2076

<210> 164
<211> 476
<212> PRT
<213> *Homo sapiens*

<400> 164
Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65	70	75	80
Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Pro Ala Gln			
85	90	95	
Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro			
100	105	110	
Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val			
115	120	125	
Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr			
130	135	140	
Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser			
145	150	155	160
Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala			
165	170	175	
Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu			
180	185	190	
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys			
195	200	205	
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg			
210	215	220	
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser			
225	230	235	240
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile			
245	250	255	
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His			
260	265	270	
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu			
275	280	285	
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr			
290	295	300	
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys			
305	310	315	320
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro			
325	330	335	
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly			
340	345	350	

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly His
 435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg
 450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
 465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 165

ttccatgccca cctaaggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

```

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 167
agctctcaga ggctggcat aggg

<210> 168
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 168
gtcggccctt tcccaggact gaacatgaag agttatgccg gtttcctcac 50

<210> 169
<211> 2477
<212> DNA
<213> Homo sapiens

<400> 169
cgagggctt tccggctccg gaatggcaca tgtggaaatc ccagtcttgt tggctacaac 60
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tcttgctgga gaagaaaggc ctgagggcag acgagggcac tctcaactcag ggtgaccagc 180
tccttgccctc tctgtggata acagagcatg agaaaagtgaa gagatgcagc ggagttaggt 240
gatggaaagtc taaaatagga aggaattttg tgtgcaatat cagactctgg gacgaggatg 300
cctggagagc ctgggggagg gcctgctaa caagcttca aaaaacagga gcgacttcca 360
ctgggctggg ataagacgtg ccggtaggat agggaaagact gggtttagtc ctaatatcaa 420
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gagaaagtat gtaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660
accaggatgg ggaccctggg tcagggcagc ctcttgcctc ctccccggaaa ttattttgg 720
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cagatgagca cacacaggag ccgttcctc accggccccc ctctcagcat ggaacagagg 840
cagccctggc cccggggccct ggaggtggac acggcgtctg tggctctgct ctcagtggc 900
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ggtgtggcca tcaactccgc tggagacctc ttctacacat cacgcacatc gccggctctgc 1680

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aggggttaat	tttgtgactt	agcttcttagc	tacttcctcc	agccatcagt	cattgggtat	2400
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acatctgcaa	aagcaaa					2477

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

Met	Gly	Thr	Leu	Gly	Gln	Ala	Ser	Leu	Phe	Ala	Pro	Pro	Gly	Asn	Tyr
1				5					10					15	

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
20 25 30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
35 40 45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
50 55 60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
65 70 75 80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
85 90 95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
 100 105 110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
 115 120 125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
130 135 140

Asn	Lys	Ser	Arg	Tyr	Pro	Pro	Leu	Ile	Val	Gln	Pro	Cys	Ser	Glu	Val
145					150					155					160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
165 170 175

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys
 180 185 190
 Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
 195 200 205
 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly
 210 215 220
 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
 225 230 235 240
 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys
 245 250 255
 Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His
 260 265 270
 Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala
 275 280 285
 Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly
 290 295 300
 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val
 305 310 315 320
 Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg
 325 330 335
 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe
 340 345 350
 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr
 355 360 365
 Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser
 370 375 380
 Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr
 385 390 395 400
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala
 405 410 415
 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
 420 425 430
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr
 435 440 445
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

100

450 455 460
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr
465 470 475 480
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly
485 490 495
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val
500 505 510
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys
515 520 525
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln
530 535 540
Leu Tyr Phe Leu Gly Glu Gln Arg
545 550

<210> 171
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 171
tggaataaccg cctcctgcag 20

<210> 172
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 172
cttctgccct ttggagaaga tggc 24

<210> 173
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 173
 ggactcactg gcccaggcct tcaatatcac cagccaggac gat 42

 <210> 174
 <211> 3106
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> modified_base
 <222> (1683)
 <223> a, t, c or g

 <400> 174
 aggctcccgc gcgcggctga gtgcggactg gagtggaaac ccgggtcccc gcgcttagag 60
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 tgctggtcgt ctgggcttc ctggtgcctc gcaggctgga ctggagcacc ctggccctc 180
 tgcggctccg ccatcgacag ctggggctgc aggccaaggg ctggaacttc atgctggagg 240
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 cgtggaacct gcatgagcca gaaagaggca aatttgactt ctctggaaac ctggacctgg 420
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gaagtgtgtc	caagtccgca	tttgagccctt	gttctggggc	ccagccaaac	acctggcttg	3060
ggctcaactgt	cctgagttgc	agtaaaagcta	taaccttcaa	tcacaa		3106

<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (539)

<223> Any amino acid

<400> 175

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20 25 30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
35 40 45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
50 55 60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
65 70 75 80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
85 90 95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
100 105 110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
115 120 125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
130 135 140

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
 145 150 155 160
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp
 165 170 175
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro
 180 185 190
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp
 195 200 205
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile
 210 215 220
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly
 225 230 235 240
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu
 245 250 255
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro
 260 265 270
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly
 275 280 285
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala
 290 295 300
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly
 305 310 315 320
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys
 325 330 335
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly
 340 345 350
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile
 355 360 365
 Ser Gly Ile Pro Leu Pro Pro Pro Asp Leu Leu Pro Lys Met Pro
 370 375 380
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu
 385 390 395 400
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu
 405 410 415
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His
 435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp
 450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val
 465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn
 485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp
 500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser
 515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr
 530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr
 545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val
 565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln
 580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln
 595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
 610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
 625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

ggggacgcgg agctgagagg ctccgggcta gctaggtgta ggggtggacg ggtcccagga 60
 ccctggtgag ggttctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120
 aaggggagca aagccgggct cggcccgagg cccccaggac ctccatctcc caatgttgaa 180
 ggaatccgac acgtgacggt ctgtccgccc tctcagacta gaggagcgct gtaaacgcca 240
 tggctcccaa gaagctgtcc tgccctcggt ccctgctgct gccgctcagc ctgacgctac 300
 tgctgccccca ggcagacact cggtcggtcg tagtgatag gggtcatgac cggttctcc 360
 tagacggggc cccgttccgc tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

tgctttggc cgaccggc ttgaagatgc gatggagcgg cctcaacgcc atacagttt 480
 atgtgccctg gaactaccac gagccacagc ctggggctta taactttat ggcagccgg 540
 acctcattgc ctttctgaat gaggcagtc tagcgaacct gttggtcata ctgagaccag 600
 gaccttacat ctgtcagag tggagatgg ggggtctccc atccctggtt cttcgaaaac 660
 ctgaaattca tctaagaacc tcagatccag acttccttgc cgcaatggac tcctggttca 720
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<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

Met	Ala	Pro	Lys	Lys	Leu	Ser	Cys	Leu	Arg	Ser	Leu	Leu	Leu	Pro	Leu
1					5				10					15	

Ser	Leu	Thr	Leu	Leu	Leu	Pro	Gln	Ala	Asp	Thr	Arg	Ser	Phe	Val	Val
					20				25				30		

Asp	Arg	Gly	His	Asp	Arg	Phe	Leu	Leu	Asp	Gly	Ala	Pro	Phe	Arg	Tyr
					35				40				45		

Val	Ser	Gly	Ser	Leu	His	Tyr	Phe	Arg	Val	Pro	Arg	Val	Leu	Trp	Ala
					50				55			60			

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe
 65 70 75 80

Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe
 85 90 95

Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala
 100 105 110

Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp
 115 120 125

Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His
 130 135 140

Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe
 145 150 155 160

Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly
 165 170 175

Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala
 180 185 190

Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu
 195 200 205

Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu
 210 215 220

Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Val Asp Phe Gly Pro
 225 230 235 240

Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro
 245 250 255

His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr
 260 265 270

Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly
 275 280 285

Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe
 290 295 300

His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly
 305 310 315 320

Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser
 325 330 335

Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

CDS CDP ECD PDE

107

340

345

350

Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro
355 360 365

Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu
370 375 380

Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu
385 390 395 400

Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr
405 410 415

Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val
420 425 430

Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val
435 440 445

Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr
450 455 460

Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg
465 470 475 480

Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro
485 490 495

Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu
500 505 510

Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys
515 520 525

Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr
530 535 540

Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly
545 550 555 560

Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr
565 570 575

Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu
580 585 590

Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu
595 600 605

Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu
610 615 620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His
 645 650

<210> 178
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 178
tggctactcc aagaccctgg catg 24

<210> 179
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 179
tggacaaatc cccttgctca gccc 24

<210> 180
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 180
gggcattcacc gaagcagtgg acctttatgg tgaccacctg atgtccaggg 50

<210> 181
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 181
ccagctatga ctatgatgca cc 22

<210> 182
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 182
tggcacccag aatggtgttg gctc 24

<210> 183
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 183
cgagatgtca tcagcaagtt ccaggaagtt cctttgggac cttaacctcc 50

<210> 184
<211> 1947
<212> DNA
<213> Homo sapiens

<400> 184
gctttgaaca cgctcgcaag cccaaagtt agcatctgat tggttatgag gtatttgagt 60
gcacccacaa tatggcttac atgttgaaaa agcttctcat cagttacata tccattattt 120
gtgttttatgg ctttatctgc ctctacactc tcttctgggtt attcaggata ccttgaagg 180
aatattcttt cgaaaaagtc agagaagaga gcagttttag tgacattcca gatgtcaaaa 240
acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcgtt 300
ttggtgtgtt cttgtcagaa gttagtgaaa ataaacttag ggaaattagt ttgaaccatg 360
agtggacatt tgaaaaactc aggcaagcaca tttcacgcaa cgcccaggac aagcaggagt 420
tgcatctgtt catgctgtcg ggggtgccccg atgctgtctt tgacettaca gacctggatg 480
tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540
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aaaacaataa gatgatagga cttgaatctc tccgagaggt gcggcacctt aagattctcc 780
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 ttgcaaatgg gatttaaact aagataatat atgcacagtg atgtgcagga acaacttcct 1620
 agattgcaag tgctcacgta caagttatta caagataatg catttttagga gtagatacat 1680
 cttttaaat aaaacagaga ggatgcata gaggctgata gaagacataa ctgaatgttc 1740
 aatgttgta gggtttaag tcattcatt ccaaattcatt ttttttttc ttttgggaa 1800
 agggaggaa aaattataat cactaatctt gttctttt aaattgttt taacttggat 1860
 gctgccgcta ctgaatgttt acaaattgct tgccctgctaa agtaaatgat taaattgaca 1920
 ttttcttact aaaaaaaaaaaaaaaa 1947

<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

Met	Ala	Tyr	Met	Leu	Lys	Lys	Leu	Leu	Ile	Ser	Tyr	Ile	Ser	Ile	Ile
1				5				10					15		

Cys	Val	Tyr	Gly	Phe	Ile	Cys	Leu	Tyr	Thr	Leu	Phe	Trp	Leu	Phe	Arg
					20			25					30		

Ile	Pro	Leu	Lys	Glu	Tyr	Ser	Phe	Glu	Lys	Val	Arg	Glu	Glu	Ser	Ser
					35		40				45				

Phe	Ser	Asp	Ile	Pro	Asp	Val	Lys	Asn	Asp	Phe	Ala	Phe	Leu	Leu	His
			50			55				60					

Met	Val	Asp	Gln	Tyr	Asp	Gln	Leu	Tyr	Ser	Lys	Arg	Phe	Gly	Val	Phe
	65					70				75			80		

Leu	Ser	Glu	Val	Ser	Glu	Asn	Lys	Leu	Arg	Glu	Ile	Ser	Leu	Asn	His
				85					90				95		

Glu	Trp	Thr	Phe	Glu	Lys	Leu	Arg	Gln	His	Ile	Ser	Arg	Asn	Ala	Gln
			100				105					110			

Asp	Lys	Gln	Glu	Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Val	Pro	Asp	Ala
				115			120				125				

Val	Phe	Asp	Leu	Thr	Asp	Leu	Asp	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro
	130				135					140					

Glu	Ala	Lys	Ile	Pro	Ala	Lys	Ile	Ser	Gln	Met	Thr	Asn	Leu	Gln	Glu
	145					150			155			160			

Leu	His	Leu	Cys	His	Cys	Pro	Ala	Lys	Val	Glu	Gln	Thr	Ala	Phe	Ser
			165				170			170			175		

Phe	Leu	Arg	Asp	His	Leu	Arg	Cys	Leu	His	Val	Lys	Phe	Thr	Asp	Val
	180					185					185			190	

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu
 195 200 205

Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu
 210 215 220

Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser
 225 230 235 240

Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu
 245 250 255

Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn
 260 265 270

Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys
 275 280 285

Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln
 290 295 300

Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile
 305 310 315 320

Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn
 325 330 335

Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu
 340 345 350

Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val
 355 360 365

Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile
 370 375 380

Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu
 385 390 395 400

His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys
 405 410 415

Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser
 420 425 430

Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu
 435 440 445

Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg
 450 455 460

Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465 470 475 480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro
485 490 495

Phe Ala Asn Gly Ile
500

<210> 186
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 186
cctccctcta ttacccatgt c 21

<210> 187
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 187
gaccaacttt ctctgggagt gagg 24

<210> 188
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 188
gtcactttat ttctctaaca acaagctcg a tccattacca gtggcag 47

<210> 189
<211> 2917
<212> DNA
<213> Homo sapiens

<400> 189
ccccacgcgtc cggccttctc tctggacttt gcatttccat tcctttcat tgacaaaactg 60
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aaqacatttq tqttttacac acataaaqat ctgtgtttgg ggtttcttct tccctccctg 180

tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgct 240
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cagattattg tgaagtgtga aatgggacat aattctacag tggagataat atacataaca 2100
gaagatgtatg taatacaag tcaaaatgca ctgggcaaat ataacaccag catggcttt 2160
tttgaatcca attcatttga aaagactata ctgtatcac catattatgt ggatttgaac 2220
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gaaactccaa accagcctt caacagtgtg catctgtttt cttcatggt tctagctctg 2700
aatgtggatgatg ctgtagcgac aatcacagtg aggcatTTG taaatcaacg ggcagactac 2760
aaataccaga agctgcagaa ctattaacta acagggtccaa ccctaagtga gacatgtttc 2820
tccaggatgc caaaggaaat gctacctcgt ggctacacat attatgaata aatgagggaa 2880
ggcctgaaag tgacacacag gcctgcgt aaaaaaaaaaaaaaa 2917

<210> 190
<211> 607
<212> PRT
<213> *Homo sapiens*

<400> 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser
 1 5 10 15
 Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys
 20 25 30
 Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met
 35 40 45
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
 50 55 60
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp
 65 70 75 80
 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr
 85 90 95
 Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr
 100 105 110
 Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile Val
 115 120 125
 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe
 130 135 140
 Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr
 145 150 155 160
 Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu
 165 170 175
 Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile
 180 185 190
 Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys
 195 200 205
 Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu
 210 215 220
 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser
 225 230 235 240
 Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg
 245 250 255
 Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr
 260 265 270
 Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys
 275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys
 290 295 300

Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val
 305 310 315 320

Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile
 325 330 335

Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val
 340 345 350

Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly
 355 360 365

His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile
 370 375 380

Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe
 385 390 395 400

Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val
 405 410 415

Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp
 420 425 430

Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser
 435 440 445

Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg
 450 455 460

Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe
 465 470 475 480

Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu
 485 490 495

Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys
 500 505 510

Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys
 515 520 525

Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg
 530 535 540

Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu
 545 550 555 560

Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

565	570	575
-----	-----	-----

Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe		
580	585	590

Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr		
595	600	605

<210> 191

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 191

tctctattcc aaactgtggc g

21

<210> 192

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 192

tttgatgacg attcgaaggt gg

22

<210> 193

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 193

ggaaggatcc ttcaccagcc ccaattaccc aaagccgcac cctgagc

47

<210> 194

<211> 2362

<212> DNA

<213> Homo sapiens

<400> 194

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cgggacatgc ggccccagga gctccccagg ctcgcgttcc cgttgctgct gttgctgttg 120
ctgctgctgc cgccgcccgttgcacagcgcca cgcgcgttca ccccacctgg 180

gagtcctcgg acgcccggca gctgcccgcg tggtttgc acc aggccaagtt cggcatcttc 240
atccactggg gaggttttc cgtgcccagc ttccggtagcg agtggttctg gtggatttg 300
caaaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattaccc tcctagttc 360
aaatatgaag attttggacc actattaca gaaaaatttt ttaatgccaa ccagtgggca 420
gatattttc aggccctctgg tgccaaatac attgtcttaa cttccaaaca tcatgaaggc 480
tttaccttgt ggggttcaga atattcgtgg aactggaatg ccatagatga ggggccccaaag 540
aggcacattg tcaaggaact tgaggtagcc attaggaaca gaactgaccc gcgttttgg 600
ctgtactatt cccttttga atggttcat ccgtctttcc ttgaggatga atccagtca 660
ttccataaagc ggcaatttcc agtttctaag acattgccag agctctatga gttagtgaac 720
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taaactcatt gtgcaaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu

1

5

10

15

Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
20 25 30

20

25

30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
35 40 45

-
35

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe
 50 55 60

Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
 65 70 75 80

Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro
 85 90 95

Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe
 100 105 110

Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr
 115 120 125

Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser
 130 135 140

Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp
 145 150 155 160

Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg
 165 170 175

Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu
 180 185 190

Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys
 195 200 205

Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val
 210 215 220

Leu Trp Ser Asp Gly Asp Gly Ala Pro Asp Gln Tyr Trp Asn Ser
 225 230 235 240

Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr
 245 250 255

Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly
 260 265 270

Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro
 275 280 285

His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr
 290 295 300

Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val
 305 310 315 320

Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn
 325 330 335

TRANSLATED SEQUENCE

119

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
450 455 460

Asn Val Ile
465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 196

tggtttgacc aggccaagtt cggt

23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 197

ggatttcatcc tcaaggaaga gcgg

24

<210> 198

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 198
 aacttgcagc atcagccact ctgc 24

<210> 199
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 199
 ttccgtgccc agcttcggt a gcgagtggtt ctgggtggat tggca 45

<210> 200
 <211> 2372
 <212> DNA
 <213> Homo sapiens

<400> 200
 agcaggaaaa tccggatgtc tcggatgtatga agtggaggcag tgagtgttag cctcaacata 60
 gttccagaac tctccatccg gactagttat tgagcatctg cctctcatat caccagtggc 120
 catctgaggt gtttccctgg ctctgaaggg gtggcacgta tgccagggtg cttcagcctg 180
 gtgttgcttc tcacttcattt ctggaccacg aggctcctgg tccaaggctc tttgcgtgca 240
 gaagagctt ccatccaggt gtcatgcaga attatggggta tcacccttgt gagcaaaaag 300
 gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgtc gggactaagt 360
 ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420
 ggctgggttgg gagatggatt cgtggtcattc tctaggatttta gcccaaaccg caagttgggg 480
 aaaaatgggg tgggtgtcctt gatttggaaat gttccagtga gccgacagt tgcagcctat 540
 ttttacaactt catctgatac ttggactaacat tcgtgcattt cagaaatttat caccacccaa 600
 gatccccat tcaacactca aactgcaaca caaacaacag aattttattgt cagtgacagt 660
 acctactcggttggcatcccc ttactctaca atacctgccc ctactactac tcctcctgt 720
 ccagcttcca cttcttattcc acggagaaaaaa aaatttggattt gtgtcacaga agttttatg 780
 gaaactagca ccatgtctac agaaactgaa ccattttgttggaaaataaaagc agcatcaag 840
 aatgaagctg ctgggtttgg aggtgtcccc acggctctgc tagtgcgttgc tctcccttcc 900
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 aggaaatata ctttacaag taacaaaaat aaaaactctt ataaatttctt attttatct 1920
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 gactaatctt attcatttc tctaataatgg caaccattat aaccttaatt tattattaac 2220
 atacctaaga agtacattgt tacctctata taccaagca cattttaaaa gtgccattaa 2280
 caaatgtatc actagccctc cttttccaa caagaaggaa ctgagagatg cagaatattt 2340
 tgtgacaaaaa aattaaagca tttagaaaaac tt 2372

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

Met	Ala	Arg	Cys	Phe	Ser	Leu	Val	Leu	Leu	Leu	Thr	Ser	Ile	Trp	Thr
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Thr	Arg	Leu	Leu	Val	Gln	Gly	Ser	Leu	Arg	Ala	Glu	Glu	Leu	Ser	Ile
				20				25						30	

Gln	Val	Ser	Cys	Arg	Ile	Met	Gly	Ile	Thr	Leu	Val	Ser	Lys	Lys	Ala
					35			40					45		

Asn	Gln	Gln	Leu	Asn	Phe	Thr	Glu	Ala	Lys	Glu	Ala	Cys	Arg	Leu	Leu
				50			55			60					

Gly	Leu	Ser	Leu	Ala	Gly	Lys	Asp	Gln	Val	Glu	Thr	Ala	Leu	Lys	Ala
				65			70			75				80	

Ser	Phe	Glu	Thr	Cys	Ser	Tyr	Gly	Trp	Val	Gly	Asp	Gly	Phe	Val	Val
					85				90					95	

Ile	Ser	Arg	Ile	Ser	Pro	Asn	Pro	Lys	Cys	Gly	Lys	Asn	Gly	Val	Gly
					100			105						110	

Val	Leu	Ile	Trp	Lys	Val	Pro	Val	Ser	Arg	Gln	Phe	Ala	Ala	Tyr	Cys
					115			120						125	

Tyr	Asn	Ser	Ser	Asp	Thr	Trp	Thr	Asn	Ser	Cys	Ile	Pro	Glu	Ile	Ile
					130			135					140		

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr
 145 150 155 160

Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser
 165 170 175

Thr Ile Pro Ala Pro Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser
 180 185 190

Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
 195 200 205

Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
 210 215 220

Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu
 225 230 235 240

Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe
 245 250 255

Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn
 260 265 270

Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
 275 280 285

Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
 290 295 300

Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
 305 310 315 320

Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 202

gagctttcca tccagggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 203
gtcagtgaca gtacctactc gg 22

<210> 204
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 204
tggagcagga ggagtagtag tagg 24

<210> 205
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 205
aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt 50

<210> 206
<211> 1620
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (973)
<223> a, t, c or g

<220>
<221> modified_base
<222> (977)
<223> a, t, c or g

<220>
<221> modified_base
<222> (996)
<223> a, t, c or g

<220>
<221> modified_base

<222> (1003)

<223> a, t, c or q

<400> 206

agatggcggt cttggcacct ctaattgctc tgggttattc ggtgcgcga ctttcacgat 60
ggctcgccca accttactac cttctgtcgg ccctgctctc tgctgccttc ctactcgta 120
ggaaaactgcc gcccgtctgc cacggctctgc caacccaacg cgaagacggt aaccctgtg 180
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acatactccc cacacccaaat tttttttttt tttttttttt tttttttttt 1620

<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
1 5 10 15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
20 25 30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
35 40 45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
50 55 60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
65 70 75 80

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
 85 90 95

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
 100 105 110

Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
 115 120 125

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys
 130 135 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val
 145 150 155 160

Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile
 165 170 175

Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly
 180 185 190

Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val
 195 200 205

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln
 210 215 220

Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg
 225 230 235 240

Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn
 245 250 255

Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp
 260 265 270

Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser
 275 280 285

Asp Gly Glu Asn Lys Lys Asp Lys
 290 295

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 208

gcttggatat tcgcatggc ctac

<210> 209
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 209
 tggagacaat atccctgagg 20

<210> 210
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 210
 aacagttggc cacagcatgg cagg 24

<210> 211
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 211
 ccattgtga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212
 <211> 1985
 <212> DNA
 <213> Homo sapiens

<400> 212
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 aaaaaa 1985

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

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5

10

15

Gly	Leu	Pro	Phe	Tyr	Asn	Gly	Phe	Tyr	Tyr	Ser	Asn	Ser	Ala	Asn	Asp
20															

25

30

Gln	Asn	Leu	Gly	Asn	Gly	His	Gly	Lys	Asp	Leu	Leu	Asn	Gly	Val	Lys
35															

35

40

45

Leu	Val	Val	Glu	Thr	Pro	Glu	Glu	Thr	Leu	Phe	Thr	Tyr	Gln	Gly	Ala
50															

50

55

60

Ser	Val	Ile	Leu	Pro	Cys	Arg	Tyr	Arg	Tyr	Glu	Pro	Ala	Leu	Val	Ser
65															

65

70

75

80

Pro	Arg	Arg	Val	Arg	Val	Lys	Trp	Trp	Lys	Leu	Ser	Glu	Asn	Gly	Ala
85															

85

90

95

Pro	Glu	Lys	Asp	Val	Leu	Val	Ala	Ile	Gly	Leu	Arg	His	Arg	Ser	Phe
100															

100

105

110

Gly	Asp	Tyr	Gln	Gly	Arg	Val	His	Leu	Arg	Gln	Asp	Lys	Glu	His	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115	120	125
Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr		
130	135	140
Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu		
145	150	155
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg		
165	170	175
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala		
180	185	190
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly		
195	200	205
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr		
210	215	220
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro		
225	230	235
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp		
245	250	255
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu		
260	265	270
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu		
275	280	285
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys		
290	295	300
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser		
305	310	315
320		
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu		
325	330	335
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr		
340	345	350
Gly Val Tyr Cys Tyr Arg Gln His		
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<210> 214

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 214
tgcttcgcta ctgccctc 18

<210> 215
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 215
ttcccttgtg ggttggag 18

<210> 216
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 216
agggctggaa gccagttc 18

<210> 217
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 217
agccagttag gaaaatgcg 18

<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 218
tgtccaaagt acacacacct gagg 24

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<210> 219
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 219
gatgccacga tcgccaagg gggacagctc tttgccgcct ggaag 45

<210> 220
<211> 1503
<212> DNA
<213> Homo sapiens

<400> 220
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tggccagggg agggtgcacc aggcggccccc cctgagcgcac gctcccatg atgacgccc 180
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aaa 1503

<210> 221
<211> 328
<212> PRT
<213> Homo sapiens

<400> 221
Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Arg His

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Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala			
35	40	45	
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val			
50	55	60	
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu			
65	70	75	80
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp			
85	90	95	
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg			
100	105	110	
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp			
115	120	125	
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly			
130	135	140	
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr			
145	150	155	160
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp			
165	170	175	
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu			
180	185	190	
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr			
195	200	205	
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu			
210	215	220	
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Pro Ala			
225	230	235	240
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn			
245	250	255	
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro			
260	265	270	
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu			
275	280	285	

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu
 325

<210> 222
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 222
 cgccaggccct catggccagg 20

<210> 223
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 223
 gaaatccctgg gtaattgg 18

<210> 224
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 224
 gtgcgcggtg ctcacagctc atc 23

<210> 225
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 225
 cccccctgag cgacgctccc ccatgatgac gcccacggga actt 44

 <210> 226
 <211> 2403
 <212> DNA
 <213> Homo sapiens

 <400> 226
 ggggccttgc ctcccgcaact cgggcgcagc cgggtggatc tcgagcagggt gcggagcccc 60
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 aaa 2403

<210> 227

<211> 550
<212> PRT
<213> Homo sapiens

<400> 227
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1 5 10 15
Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile
20 25 30
Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
35 40 45
Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
50 55 60
Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
65 70 75 80
Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
85 90 95
Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
100 105 110
Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
115 120 125
Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
130 135 140
Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
145 150 155 160
Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
165 170 175
Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
180 185 190
Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
195 200 205
Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
210 215 220
Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
225 230 235 240
Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
245 250 255

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val
 260 265 270

Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val
 275 280 285

Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro
 290 295 300

Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys
 305 310 315 320

Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp
 325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr
 340 345 350

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile
 355 360 365

Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg
 370 375 380

Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser
 385 390 395 400

Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg
 405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
 420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp
 435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser
 450 455 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp
 465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala His Asp Ala Gly Ile Thr Ile
 485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met
 500 505 510

Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr
 515 520 525

Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp
 530 535 540

Phe Leu Glu Ser Gln Gln
545 550

<210> 228
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 228
tggtctcgca caccgatc 18

<210> 229
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 229
ctgcgtgtcca caggggag 18

<210> 230
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 230
ccttgaagca tactgctc 18

<210> 231
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 231
gagatagcaa tttccgccc 18

<210> 232

<211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 232
 ttcctcaaga gggcagcc 18

<210> 233
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 233
 cttggcacca atgtccgaga ttcc 24

<210> 234
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 234
 gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg 45

<210> 235
 <211> 2586
 <212> DNA
 <213> Homo sapiens

<400> 235
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Cys Ala His Pro Leu Ala Thr Leu Phe Lys Ile Leu Ala Ser Phe 50 55 60
Tyr Ile Ser Leu Val Ile Phe Tyr Gly Leu Ile Cys Met Tyr Thr 65 70 75
Leu Trp Trp Met Leu Arg Arg Ser Leu Lys Lys Tyr Ser Phe Glu 80 85 90
Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys

95	100	105
Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro		
110	115	120
Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu		
125	130	135
Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu Asp		
140	145	150
Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu		
155	160	165
Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp		
170	175	180
Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val		
185	190	195
Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu		
200	205	210
Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala		
215	220	225
Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp		
230	235	240
Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu		
245	250	255
Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr		
260	265	270
Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu		
275	280	285
Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp		
290	295	300
Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr		
305	310	315
Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr		
320	325	330
Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser		
335	340	345
Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn		
350	355	360

Asn	Leu	Lys	Thr	Ile	Glu	Glu	Ile	Ser	Phe	Gln	His	Leu	His	
				365			370					375		
Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	Tyr	Asn	His	Ile	Ala	Tyr	Ile
				380			385					390		
Pro	Ile	Gln	Ile	Gly	Asn	Leu	Thr	Asn	Leu	Glu	Arg	Leu	Tyr	Leu
				395			400					405		
Asn	Arg	Asn	Lys	Ile	Glu	Lys	Ile	Pro	Thr	Gln	Leu	Phe	Tyr	Cys
				410			415					420		
Arg	Lys	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	His	Asn	Asn	Leu	Thr	Phe
				425			430					435		
Leu	Pro	Ala	Asp	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	Asn	Leu	Ala
				440			445					450		
Ile	Thr	Ala	Asn	Arg	Ile	Glu	Thr	Leu	Pro	Pro	Glu	Leu	Phe	Gln
				455			460					465		
Cys	Arg	Lys	Leu	Arg	Ala	Leu	His	Leu	Gly	Asn	Asn	Val	Leu	Gln
				470			475					480		
Ser	Leu	Pro	Ser	Arg	Val	Gly	Glu	Leu	Thr	Asn	Leu	Thr	Gln	Ile
				485			490					495		
Glu	Leu	Arg	Gly	Asn	Arg	Leu	Glu	Cys	Leu	Pro	Val	Glu	Leu	Gly
				500			505					510		
Glu	Cys	Pro	Leu	Leu	Lys	Arg	Ser	Gly	Leu	Val	Val	Glu	Glu	Asp
				515			520					525		
Leu	Phe	Asn	Thr	Leu	Pro	Pro	Glu	Val	Lys	Glu	Arg	Leu	Trp	Arg
				530			535					540		
Ala	Asp	Lys	Glu	Gln	Ala									
				545										

<210> 251

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 251

caacaatgag ggcaccaagc 20

<210> 252

<211> 24

Sequence Database

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 252
gatggctagg ttctggaggt tctg 24

<210> 253
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 253
caacctgcag gagattgacc tcaaggacaa caacctaag accatcg 47

<210> 254
<211> 1650
<212> DNA
<213> Homo Sapien

<400> 254
gcctgttgc gatgctgccg tgccgtactt gtcatggagc tggcactg 50
gcgtctccc gtcccgccgt gtttgctgct gctgccgctg ctgctggcc 100
tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150
tgggattatg tgacggtccg caaggatgcc tacatgttct ggtggctcta 200
ttatgccacc aactcctgca agaacttctc agaactgcc ctggcatgt 250
ggcttcaggc cggtccaggc gttttagca ctggatttgg aaactttgag 300
gaaattgggc cccttgacag tggatctaaa ccacggaaaa ccacctggct 350
ccaggctgcc agtctcctat ttgtggataa tcccgtggc actgggttca 400
gttatgtgaa tggtagtggt gcctatgccc aggacctggc tatggtggt 450
tcagacatga tggttctcct gaagaccttc ttcagttgcc acaaagaatt 500
ccagacagtt ccattctaca ttttctcaga gtcctatgga ggaaaaatgg 550
cagctggcat tggtctagag ctttataagg ccattcagcg agggaccatc 600
aagtgcact ttgcgggggt tgccttgggt gattcctgga tctccctgt 650
tgattcggtg ctctcctggg gaccttacct gtacagcatg tctttctcg 700
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aagacaaagg tctggcagag gtgtctaagg ttgcagagca agtactgaat 750
 gccgtaaata aggggctcta cagagaggcc acagagctgt gggggaaagc 800
 agaaaatgatc attgaacaga acacagatgg ggtgaacttc tataacatct 850
 taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900
 cagagccacc tagttgtct ttgtcagcgc cacgtgagac acctacaacg 950
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 ttattcctga ggatcaatcc tggggaggcc aggctaccaa cgtcttg 1050
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 gggctggaga tgagctggtt tggccttggg gcacagagct gagctgaggc 1450
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 gatcaagaag gttctgacca gcttctgcag aggataaaat cattgtctct 1550
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 taaaaaaaaatg atttgtttt atcaaaaataa aggatgataa tagatattaa 1650

<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu Leu

1 5 10 15

Leu Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp

20 25 30

Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val

35 40 45

Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn
 50 55 60

 Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln
 65 70 75

 Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu
 80 85 90

 Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp
 95 100 105

 Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr
 110 115 120

 Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu
 125 130 135

 Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe
 140 145 150

 Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser
 155 160 165

 Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu
 170 175 180

 Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly
 185 190 195

 Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu
 200 205 210

 Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys
 215 220 225

 Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala
 230 235 240

 Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys
 245 250 255

 Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr
 260 265 270

 Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser
 275 280 285

 Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His
 290 295 300

 Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly

305	310	315
-----	-----	-----

Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp	320	325
---	-----	-----

Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe	335	340
---	-----	-----

Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly	350	355
---	-----	-----

Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp	365	370
---	-----	-----

Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu	380	385
---	-----	-----

Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp	395	400
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Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn	410	415
---	-----	-----

Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser	425	430
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Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln	440	445
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Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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tgctgctggc tcgggctgga ctcaggaagc cggagtgcgc ggaggcggcg 100

ccgttatcag gaccatgcgg ccgacgggtc atcacgtgcgc gcatcgtggg 150

tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200

tgtgggattc ccacgtatgc ggagtgagcc tgctcagcca ccgctggca 250

ctcacggcgg cgcaactgctt taaaacctat agtaccccta gtgatccctc 300

cgggtggatg gtccagtttgc cccagctgac ttccatgcca tccttctgga 350

gcctgcaggc ctactacacc cgttacttcg tatcaatat ctatctgagc 400

cctcgctacc tggggaattc accctatgac attgccttgg tgaagctgtc 450
 tgcacctgtc acctacacta aacacatcca gcccacatctgt ctccaggcct 500
 ccacatttga gtttgagaac cggacagact gctgggtgac tggctgggg 550
 tacatcaaag aggatgaggc actgccatct ccccacaccc tccaggaagt 600
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 tttgagtgga tccagaagct gatggcccag agtggcatgt cccagccaga 900
 cccctctgg ccactactct tttccctct tctctggct ctcccactcc 950
 tggggccggc ctgagcctac ctgagcccat gcagcctggg gccactgcca 1000
 agtcaggccc tggttctctt ctgtcttgg tggtaataaa cacattccag 1050
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<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

Met	Gly	Ala	Arg	Gly	Ala	Leu	Leu	Leu	Ala	Leu	Leu	Ala	Arg
1					5				10			15	

Ala	Gly	Leu	Arg	Lys	Pro	Glu	Ser	Gln	Glu	Ala	Ala	Pro	Leu	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20					25					30				
----	--	--	--	--	----	--	--	--	--	----	--	--	--	--

Gly	Pro	Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly	Gly
						35			40			45		

Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg
						50			55			60		

Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg
					65				70			75		

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
						80			85			90		

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser
 95 100 105

 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe
 110 115 120

 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
 125 130 135

 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
 140 145 150

 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
 155 160 165

 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys
 170 175 180

 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln
 185 190 195

 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
 200 205 210

 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly
 215 220 225

 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
 230 235 240

 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
 245 250 255

 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
 260 265 270

 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met
 275 280 285

 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu
 290 295 300

 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
 305 310

<210> 258
 <211> 2427
 <212> DNA
 <213> Homo Sapien

<400> 258
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cctcctaggg ctctttgccc tcatacctctc tggcaaatgc agttacagcc 100
cgagccccga ccagcggagg acgctgcccc caggctgggt gtccctggc 150
cgtcgccgacc ctgaggaaga gctgagtctc acctttgccc tgagacagca 200
aatgtggaa agactctcg agctggtgca ggctgtgtcg gatcccagct 250
ctcctaata cgaaaaatac ctgaccctag agaatgtggc tcatctggtg 300
aggccatccc cactgaccct ccacacggtg caaaaatggc tcttggcagc 350
cgagccccag aagtgcatt ctgtgatcac acaggactt ctgacttgc 400
ggctgagcat ccgacaagca gagctgctgc tccctgggc tgagtttcat 450
caatatgtgg gaggacctac gaaaacccat gtttaagggt cccacatcc 500
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tgcaccgttt tcccccaaca tcataccctga ggcaacgtcc tgagccgcag 600
gtgacagggta ctgttaggcct gcatctgggg gtaacccct ctgtgatccg 650
taagcgatac aacttgacct cacaagacgt gggctctggc accagcaata 700
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ccagtctaga tgtgcagttac ctgatgagtg ctggtgccaa catctccacc 900
tgggtctaca gtagccctgg cccggcatgag ggacaggagc cttccctgca 950
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gtcaacactg agctcatgaa ggctgccgct cggggctca ccctgtctt 1100
cgcttcaggt gacagtgggg ccgggtgttg gtctgtctt ggaagacacc 1150
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agttacttca atgccagtgccgtcctac ccagatgtgg ctgcacttcc 1400

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 ccttacttag cttccaggc ttaacttctc tgactactct tgtcttcctc 2250
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 tgttagattt tgctcttc agtttactca ttgtccctg gaacaaatca 2350
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<210> 259
 <211> 556
 <212> PRT
 <213> Homo Sapien

<400> 259
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Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu		
35	40	45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg		
50	55	60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln		
65	70	75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg		
80	85	90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala		
95	100	105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu		
110	115	120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly		
125	130	135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val		
140	145	150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro		
155	160	165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser		
170	175	180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly		
185	190	195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn		
200	205	210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln		
215	220	225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu		
230	235	240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala		
245	250	255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly		
260	265	270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala		
275	280	285

Asn Ile Ser Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly
 290 295 300
 Gln Glu Pro Phe Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser
 305 310 315
 Ala Leu Pro His Val His Thr Val Ser Tyr Gly Asp Asp Glu Asp
 320 325 330
 Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val Asn Thr Glu Leu Met
 335 340 345
 Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp
 350 355 360
 Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His Gln Phe Arg
 365 370 375
 Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val Gly Gly
 380 385 390
 Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val Asp
 395 400 405
 Tyr Ile Ser Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser
 410 415 420
 Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His
 425 430 435
 Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro
 440 445 450
 Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg
 455 460 465
 Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val
 470 475 480
 Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser
 485 490 495
 Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln
 500 505 510
 His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser
 515 520 525
 Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro
 530 535 540
 Gly Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Thr Ser Gln Leu
 545 550 555

Cys

<210> 260
<211> 1638
<212> DNA
<213> Homo Sapien

<400> 260
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cgccggccgg gcgggctgct cggcgccgaa cagtgc tgg catggcagg 100
atccaggc tcctcttc tctttt ctgtctgt ctgttggca 150
agt gaccc tacagtgc cctggaaacc cacttggct gcataaccgcc 200
tccctgtcgt cttgccccag tctaccctca atttagccaa gccagactt 250
ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300
taaggaaact ccactgccc cttacgaaga ggccaagcaa tatctgtctt 350
atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcatc 400
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ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcagg 500
tcagcattt tggaaaggac ttccctgctca actaccctt ctaacatca 550
gtaaagttat ccacggcgtg caccggcacc ctgggtggcag agaagcatgt 600
cctcacagct gcccactgca tacacgatgg aaaaacctat gtgaaaggaa 650
cccagaagct tcgagtgccc ttccctaaagc ccaagttaa agatgggtggt 700
cgaggggcca acgactccac ttca gggccatg cccgagcaga tgaaatttca 750
gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaaggcga 800
atgccaatga catcgccatg gattatgatt atgcccctt ggaactcaaa 850
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctccctgctaa 900
gcagctgcca gggggcagaa ttca gtttgcac aatgaccgac 950
caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000
ttgctctacc agcaatgcga tgcccgccca ggggcccagcg ggtctggggt 1050
ctatgtgagg atgtgaaaga gacagcagca gaagtgggag cgaaaaattha 1100

!-----!
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!-----!

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<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Leu	Leu
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Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro
				20					25					30

Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr
				35					40					45

Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu
				50					55					60

Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu
				65					70					75

Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu
					80				85					90

Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile
						95				100				105

Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser
				110					115					120

Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser
 125 130 135
 Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe
 140 145 150
 Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val
 155 160 165
 Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly
 170 175 180
 Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu
 185 190 195
 Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr
 200 205 210
 Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys
 215 220 225
 Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
 230 235 240
 Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro
 245 250 255
 His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys
 260 265 270
 Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp
 275 280 285
 Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu
 290 295 300
 Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala
 305 310 315
 Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln
 320 325 330
 Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp
 335 340 345
 Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg
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 Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly
 365 370 375
 Asn Tyr Leu Asp Cys Arg Glu Gly
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<210> 262
<211> 1378
<212> DNA
<213> Homo Sapien

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caggataacct gttccccccag cctgtggaa gccccagcag ctgaaccggg 200
ttgtggcgcc cgaggacacgc actgacagcg agtggccctg gatcgtgagc 250
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ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350
acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400
cggtcccaga aggtgggtgt tgccctgggtg gagccccacc ctgtgtattc 450
ctggaaggaa ggtgcctgtg cagacattgc cctggtgctg ctgcagcgt 500
ccatacagtt ctcagagcgg gtcctgccc tctgcctacc tgatgcctct 550
atccacactcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600
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<210> 263

<211> 317

<212> PRT

<213> Homo Sapien.

<400> 263

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Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu	
				20					25			30		
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln
				35					40			45		
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glut
				50					55			60		
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys
				65					70			75		
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His
				80					85			90		
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu
				95					100			105		
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys
				110					115			120		
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys
				125					130			135		
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser
				140					145			150		
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala
				155					160			165		
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp
				170					175			180		

Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu
 185 190 195

 Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His
 200 205 210

 Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met
 215 220 225

 Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
 230 235 240

 Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu
 245 250 255

 Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn
 260 265 270

 Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val
 275 280 285

 Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly
 290 295 300

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 305 310 315

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gttc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaagggtt 19

<210> 266

<211> 24

1000 900 800 700 600 500 400 300 200 100

<212> DNA

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<223> Synthetic Oligonucleotide Probe

<400> 266

agctctagac caatgccagc ttcc 24

<210> 267

<211> 45

<212> DNA

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gccaccaact cctgcaagaa ctttcagaa ctgcccctgg tcatg 45

<210> 268

<211> 25

<212> DNA

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<400> 268

gggaaattca ccctatgaca ttgcc 25

<210> 269

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 269

aatgccttg caagcatcaa ctgg 24

<210> 270

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 270

gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

170

<210> 271
<211> 26
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<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 271
gcggaagggc agaatgggac tccaaag 26

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 272
cagccctgcc acatgtgc 18

<210> 273
<211> 18
<212> DNA
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<220>
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<400> 273
tactgggtgg tcagcaac 18

<210> 274
<211> 24
<212> DNA
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<400> 274
ggcgaagagc agggtgagac cccg 24

<210> 275
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

THERMUS

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<220>
<223> Synthetic Oligonucleotide Probe

<400> 276
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<210> 277
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 277
ggctatgaca gcaggttc 18

<210> 278
<211> 18
<212> DNA
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<223> Synthetic Oligonucleotide Probe

<400> 278
tgacaatgac cgaccagg 18

<210> 279
<211> 24
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 279
gcatcgatt gctggtagag caag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
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<223> Synthetic Oligonucleotide Probe

<400> 280
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<210> 281
<211> 34
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281
cgtctcgagc gtcataaca gttcccttgc ccca 34

<210> 282
<211> 61
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282
tggaggggga gcgggatgct tgtctggcg actccggggg cccccctcatg 50
tgccaggtgg a 61

<210> 283
<211> 119
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283
ccctcagacc ctgcagaagc tgaagggttcc tatcatcgac tcggaagtct 50
gcagccatct gtactggcg ggagcaggac agggacccat cactgaggac 100
atgctgtgtg ccggctact 119

<210> 284
<211> 1875
<212> DNA
<213> Homo Sapien

<400> 284
gacggctggc caccatgcac ggctcctgca gttccctgat gtttctgt 50
ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgttga tggtagatc gcacaacctc taccgggccc 150
aggatatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200
ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt gggccacaa 250
caaggagcgc gggcgccgag gcgagaatct gttcgccatc acagacgagg 300
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ataaaaacct gtccaaacctg tgaaa 1875

<210> 285
<211> 463
<212> PRT
<213> Homo Sapien

<400> 285
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Glu Glu Lys Arg Leu Met Val Glu Leu His Asn Leu Tyr Arg Ala
35 40 45
Gln Val Ser Pro Thr Ala Ser Asp Met Leu His Met Arg Trp Asp
50 55 60
Glu Glu Leu Ala Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val
65 70 75
Trp Gly His Asn Lys Glu Arg Gly Arg Arg Gly Glu Asn Leu Phe
80 85 90
Ala Ile Thr Asp Glu Gly Met Asp Val Pro Leu Ala Met Glu Glu
95 100 105
Trp His His Glu Arg Glu His Tyr Asn Leu Ser Ala Ala Thr Cys
110 115 120
Ser Pro Gly Gln Met Cys Gly His Tyr Thr Gln Val Val Trp Ala
125 130 135

TOPPEL ET AL.

Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu
140 145 150

Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr
155 160 165

Glu Pro Pro Gly Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly
170 175 180

Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser
185 190 195

Leu Cys Glu Pro Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro
200 205 210

Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser
215 220 225

Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile
230 235 240

Pro Ala Phe Leu Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys
245 250 255

Ala Leu Pro Ala Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr
260 265 270

Lys Asp Pro Pro Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr
275 280 285

Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu
290 295 300

Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile
305 310 315

Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser
320 325 330

Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly
335 340 345

Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu
350 355 360

Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro
365 370 375

Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr
380 385 390

Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser
395 400 405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser
 410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
 425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
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<223> Synthetic Oligonucleotide Probe

<400> 286

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<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

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DNA sequence

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caaggcaagt tccatgagcc accttcaaag cttcgagaa gtgaaaactga 200
acaacaatga attggagacc attccaaatc tgggaccagt ctcggcaa 250
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tttggccaac acactccttg tggtaaagct gaacaggaac cgaatctcag 500
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<212> PRT

<213> Homo Sapien

<400> 290

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20 25 30

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu		
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Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser		
50	55	60
Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu		
65	70	75
Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu		
80	85	90
Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro		
95	100	105
Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr		
110	115	120
Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu		
125	130	135
Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys		
140	145	150
Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn		
155	160	165
Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala		
170	175	180
Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met		
185	190	195
Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu		
200	205	210
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly		
215	220	225
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn		
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Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu		
245	250	255
Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser		
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Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn		
275	280	285
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser		

290	295	300
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile		
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Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
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Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
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Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
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Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
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Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
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425	430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala		
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Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser		
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Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu		
470	475	480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln		
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Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu		
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Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn		
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His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn		
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Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg		
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 Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser
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 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln
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<212> DNA

<213> Homo Sapien

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Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
														45

Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
														60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
														75

Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
														90
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
														105

Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
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Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
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Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
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Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

DRAFT

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Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp			
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<212> PRT

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Ser	Arg	Lys	Arg	Leu	Ala	Arg	Leu	Pro	Glu	Pro	Leu	Pro	Ser	Trp
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Val	Ala	Arg	Leu	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
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Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu		
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Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly		
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Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu		
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Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn		
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Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser		
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Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
410	415	420
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
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Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
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Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
455	460	465
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
470	475	480

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 710 715 720
 Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser
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 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln
 740 745 750

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 875 880 885
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
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<400> 296

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<210> 297

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<212> DNA

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 <211> 3296
 <212> DNA
 <213> Homo Sapien

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<213> Homo Sapien

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ESTATE OF LUCILLE

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 35 40 45
 Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys
 50 55 60
 Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys
 65 70 75
 Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu
 80 85 90
 Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met
 95 100 105
 Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met
 110 115 120
 Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met
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 Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg
 155 160 165

Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys
 170 175 180

 Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys
 185 190 195

 Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr
 200 205 210

 Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys
 215 220 225

 Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys
 230 235 240

 Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr
 245 250 255

 Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro
 260 265 270

 Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn
 275 280 285

 Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro
 290 295 300

 Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr
 305 310 315

 Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro
 320 325 330

 Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr
 335 340 345

 Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala
 350 355 360

 Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln
 365 370 375

 Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val
 380 385 390

 His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu
 395 400 405

 Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly
 410 415 420

 Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys

425	430	435
Ala Ala Arg Leu Val Leu Pro Leu Gly Arg	Leu Met His Ser Gly	
440	445	450
Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly	Leu His Ser	
455	460	465
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala		
470	475	480
Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln		
485	490	495

Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg
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<210> 316

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 316

gatggttcct gctcaagtgc cctg 24

<210> 317

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 317

ttgcacttgt aggaccacg tacg 24

<210> 318

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 318

ctgatggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

<210> 319

<211> 2110

<212> DNA

<213> Homo Sapien

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caacaggtgc ttgctcg(ggg) ctgaagggtga cagtgccatc acacactgtc 150
catggcgtca gaggtcaggc cctctaccta cccgtccact atggcttcca 200
cactccagca tcagacatcc agatcatatg gctatttgag agaccccaca 250
caatgccc(aa) atacttactg ggctctgtga ataagtctgt gt(t)ctgac 300
ttgaaatacc aacacaagtt caccatgtatg ccacccaaatg catctctgt 350
tatcaaccc(a) ctgcagttcc ctgatgttgg caattacatc gtgttgtca 400
acattcaggg aaatggaact ctatctgcca gtcagaagat acaagtcacg 450
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gaagacaatg gactatgtgt gctgtgttca caacaacata accggcaggc 1000
aagatgaaac tcatttcaca gttatcatca cttccgttgg actggagaag 1050
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atcactatTT ttgattatat ccatgtgtct tctcttccta tggaaaaaat 1150
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gaatacagga aagctcaaac atttcaggc catgaagatg ctctggatga 1250

cttcggaata tatgaatttg ttgctttcc agatgttct ggtgttcca 1300
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 ttctatcttg ttatttgtac aacaaagtaa taaggatggt tgtcacaaaa 1950
 acaaaactat gccttctctt tttttcaat caccagtagt atttttgaga 2000
 agacttgtga acacttaagg aaatgactat taaagtctta tttttatttt 2050
 tttcaaggaa agatggattc aaataaaatta ttctgtttt gcttttaaaa 2100
 aaaaaaaaaa 2110

<210> 320
 <211> 450
 <212> PRT
 <213> Homo Sapien

<400> 320			
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Ala Cys Ser Gly Leu Lys Val Thr Val Pro Ser His Thr Val His			
20	25	30	
Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe			
35	40	45	
His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg			
50	55	60	

Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser
 65 70 75
 Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro
 80 85 90
 Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu
 95 100 105
 Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu
 110 115 120
 Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr
 125 130 135
 Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr
 140 145 150
 Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg
 155 160 165
 Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser
 170 175 180
 Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala
 185 190 195
 Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg
 200 205 210
 Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile
 215 220 225
 Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu
 230 235 240
 Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu
 245 250 255
 Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp
 260 265 270
 Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro
 275 280 285
 Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp
 290 295 300
 Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu
 305 310 315
 Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu

320	325	330
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Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly		
335	340	345

Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp		
350	355	360

Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly		
365	370	375

Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His		
380	385	390

Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe		
395	400	405

Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro		
410	415	420

Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr		
425	430	435

Glu Val Ile Gln His Ile Pro Ala Gln Gln Asp His Pro Glu		
440	445	450

<210> 321

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 321

gatcctgtca caaagccagt ggtgc 25

<210> 322

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 322

cactgacagg gttcctcacc cagg 24

<210> 323

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

gcaagcggcg aaatggcgcc ctccgggagt cttgcagttc ccctggcagt 50

cctggtgctg ttgcttggg gtgctccctg gacgcacggg cggcggagca 100

acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150

tggatgatag aatttatgc cccgtggtgc cctgcttgc aaaatcttca 200

accggaatgg gaaagtttg ctgaatgggg agaagatctt gaggttaata 250

ttgcgaaagt agatgtcaca gaggcagccag gactgagtgg acggtttatac 300

ataactgctc ttccctactat ttatcattgt aaagatggtg aatttaggcg 350

ctatcagggc ccaaggacta agaaggactt cataaacttt ataagtgata 400

aagagtggaa gagtattgag cccgtttcat catggttgg tccaggttct 450

gttctgatga gtagtatgtc agcactctt cagctatcta tgtggatcag 500

gacgtgccat aactactta ttgaagacct tggattgcca gtgtggggat 550

catatactgt ttttgctta gcaactctgt tttccggact gttatttagga 600

ctctgtatga tatttgtggc agattgcctt tgcccttcaa aaaggcgcag 650

accacagcca taccataacc cttcaaaaaa attattatca gaatctgcac 700

aaccttgaa aaaagtggag gaggaacaag aggccgatga agaagatgtt 750

tcagaagaag aagctgaaag taaagaagga acaaacaag actttccaca 800

gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850

cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900

aagattgatc attttgggg gtttgaagtg aactgtgact tttttgaata 950

ttgcagggtt cagtctagat tgtcattaaa ttgaagagtc tacattcaga 1000

acataaaaagc actaggatata caagtttcaa atatgattta agcacagtat 1050
gatggtttaa atagttctct aatttttcaa aaatcggtcc aagcaataag 1100
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aaacctttct aaccacttca ttaaagctga aaaaaaaaaa aaaaaaaa 2397

<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

Met	Ala	Pro	Ser	Gly	Ser	Leu	Ala	Val	Pro	Leu	Ala	Val	Leu	Val
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Leu	Leu	Leu	Trp	Gly	Ala	Pro	Trp	Thr	His	Gly	Arg	Arg	Ser	Asn
														30
20										25				

Val	Arg	Val	Ile	Thr	Asp	Glu	Asn	Trp	Arg	Glu	Leu	Leu	Glu	Gly
														45
35									40					

Asp	Trp	Met	Ile	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Pro	Ala	Cys	Gln
														60
50									55					

Asn	Leu	Gln	Pro	Glu	Trp	Glu	Ser	Phe	Ala	Glu	Trp	Gly	Glu	Asp
														75
65									70					

Leu	Glu	Val	Asn	Ile	Ala	Lys	Val	Asp	Val	Thr	Glu	Gln	Pro	Gly
														90
80									85					

Leu	Ser	Gly	Arg	Phe	Ile	Ile	Thr	Ala	Leu	Pro	Thr	Ile	Tyr	His
														105
95									100					

Cys	Lys	Asp	Gly	Glu	Phe	Arg	Arg	Tyr	Gln	Gly	Pro	Arg	Thr	Lys
														120
110								115						

Lys	Asp	Phe	Ile	Asn	Phe	Ile	Ser	Asp	Lys	Glu	Trp	Lys	Ser	Ile
														135
125									130					

Glu	Pro	Val	Ser	Ser	Trp	Phe	Gly	Pro	Gly	Ser	Val	Leu	Met	Ser
														150
140									145					

Ser	Met	Ser	Ala	Leu	Phe	Gln	Leu	Ser	Met	Trp	Ile	Arg	Thr	Cys
														165
155									160					

His	Asn	Tyr	Phe	Ile	Glu	Asp	Leu	Gly	Leu	Pro	Val	Trp	Gly	Ser
														180
170									175					

Tyr	Thr	Val	Phe	Ala	Leu	Ala	Thr	Leu	Phe	Ser	Gly	Leu	Leu	Leu
														195
185									190					

Gly	Leu	Cys	Met	Ile	Phe	Val	Ala	Asp	Cys	Leu	Cys	Pro	Ser	Lys
														210
200									205					

Arg	Arg	Arg	Pro	Gln	Pro	Tyr	Pro	Tyr	Pro	Ser	Lys	Lys	Leu	Leu
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	215	220	225
Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu			
230	235	240	
Ala Asp Glu Glu Asp Val Ser Glu Glu Ala Glu Ser Lys Glu			
245	250	255	
Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser			
260	265	270	
Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser			
275	280		

<210> 326

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 326

ttaggtgggc aagcggcgaa atg 23

<210> 327

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 327

tatgtggatc aggacgtgcc 20

<210> 328

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 328

tgcagggttc agtctagatt g 21

<210> 329

<211> 25

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 329
ttgaaggaca aaggcaatct gccac 25

<210> 330
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 330
ggagtcttgc agttcccttg gcagtcctgg tgctgttgct ttggg 45

<210> 331
<211> 2168
<212> DNA
<213> Homo Sapien

<400> 331
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aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taacccagtg 100
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acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200
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gttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150

cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

Met	Lys	Leu	Trp	Val	Ser	Ala	Leu	Leu	Met	Ala	Trp	Phe	Gly	Val
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Leu	Ser	Cys	Val	Gln	Ala	Glu	Phe	Phe	Thr	Ser	Ile	Gly	His	Met
			20						25					30

Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Glu	Leu	Val	Gln	Ser	Leu	Lys
			35						40				45

Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser
			50						55				60	

Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp
			65					70					75	

Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val
			80					85					90	

Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu
			95					100					105	

Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg
			110					115					120	

Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala
			125					130					135	

Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile
			140					145					150	

Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser
			155					160					165	

Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly
			170					175					180	

Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln
			185					190					195	

Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Lys	Ser	Gln	Val	Leu
			200					205					210

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg
 215 220 225
 Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His
 230 235 240
 Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu
 245 250 255
 Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu
 260 265 270
 Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro
 275 280 285
 Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys
 290 295 300
 Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His
 305 310 315
 Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu
 320 325 330
 Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met
 335 340 345
 Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys
 350 355 360
 Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr
 365 370 375
 Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp
 380 385 390
 Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile
 395 400 405
 Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn
 410 415 420
 Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg
 425 430 435
 Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala
 440 445 450
 Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr
 455 460 465
 Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr
 470 475 480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr
485 490 495
Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
500 505 510
Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg
515 520 525
Pro Cys Gly Ser Thr Glu Val Asp
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<210> 333
<211> 18
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<213> Artificial Sequence

<220>
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<400> 333
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<210> 334
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<220>
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<400> 334
ggacccttct gtgtgccag 19

<210> 335
<211> 19
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<220>
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<400> 335
ggtctcaaga actcctgtc 19

<210> 336
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<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 336
acactcagca ttgcctggta cttg 24

<210> 337
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
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<400> 337
ggcacatga ctgacacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338
<211> 2789

<212> DNA
<213> Homo Sapien

<400> 338
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tcccaagtgtg agtcaaattt attgtttcat ttattaccgt tttggctggg 100
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agacaggaca atcttcttgg ggatgctggt cctggaaagcc agcgggcctt 200
gctctgtctt tggcctcatt gaccccaggt tctctggta aaactgaaag 250
cctactactg gcctggtgcc catcaatcca ttgatccttg aggctgtgcc 300
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ttggctctgc tgccggccagc gcttccccctc atcttagggc tgtctctggg 400
gtcaaggctg agcctctgc gggtttctg gatccagggg gagggagaag 450
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 cgactacgac tggttttca tcatgcagga tgacacatata gtcaggccc 900
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 gcccgcctgg gggccctaac ctcattaccc ttcccttgc tgcctcagcc 2700
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 ttttaata tgaaaatgtt attaaacatg tcttcgtcc 2789

<210> 339
 <211> 772
 <212> PRT
 <213> Homo Sapien

<400> 339
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 35 40 45
 Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg
 50 55 60
 Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr
 65 70 75
 Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Lys Val Leu Arg Thr Arg
 80 85 90
 Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala

95	100	105
Val Leu Thr Ser Arg Ala Thr Leu Ser	Thr Leu Ala Val Ala Val	
110	115	120
Asn Arg Thr Val Ala His His Phe Pro Arg	Leu Leu Tyr Phe Thr	
125	130	135
Gly Gln Arg Gly Ala Arg Ala Pro Ala Gly	Met Gln Val Val Ser	
140	145	150
His Gly Asp Glu Arg Pro Ala Trp Leu Met Ser	Glu Thr Leu Arg	
155	160	165
His Leu His Thr His Phe Gly Ala Asp	Tyr Asp Trp Phe Phe Ile	
170	175	180
Met Gln Asp Asp Thr Tyr Val Gln Ala Pro Arg	Leu Ala Ala Leu	
185	190	195
Ala Gly His Leu Ser Ile Asn Gln Asp	Leu Tyr Leu Gly Arg Ala	
200	205	210
Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala Arg	Tyr Cys His Gly	
215	220	225
Gly Phe Gly Tyr Leu Leu Ser Arg Ser	Leu Leu Leu Arg Leu Arg	
230	235	240
Pro His Leu Asp Gly Cys Arg Gly Asp	Ile Leu Ser Ala Arg Pro	
245	250	255
Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp Ser	Leu Gly Val Gly	
260	265	270
Cys Val Ser Gln His Gln Gly Gln Gln Tyr Arg Ser	Phe Glu Leu	
275	280	285
Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly Ser	Ser Ala Phe Leu	
290	295	300
Ser Ala Phe Ala Val His Pro Val Ser Glu Gly	Thr Leu Met Tyr	
305	310	315
Arg Leu His Lys Arg Phe Ser Ala Leu Glu Leu	Glu Arg Ala Tyr	
320	325	330
Ser Glu Ile Glu Gln Leu Gln Ala Gln Ile Arg	Asn Leu Thr Val	
335	340	345
Leu Thr Pro Glu Gly Glu Ala Gly Leu Ser Trp	Pro Val Gly Leu	
350	355	360

Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp
 365 370 375

 Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala
 380 385 390

 Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp
 395 400 405

 Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro
 410 415 420

 Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg
 425 430 435

 Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu
 440 445 450

 Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg
 455 460 465

 Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met
 470 475 480

 Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu
 485 490 495

 Leu Val Ala Glu Ala Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe
 500 505 510

 Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu
 515 520 525

 Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp
 530 535 540

 Pro Phe Leu Gly Val Lys Ala Ala Ala Ala Glu Leu Glu Arg Arg
 545 550 555

 Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala
 560 565 570

 Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro
 575 580 585

 Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly
 590 595 600

 Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp
 605 610 615

 Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu
 620 625 630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp
 635 640 645
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile
 650 655 660
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr
 665 670 675
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu
 680 685 690
 Ala Gly Gln Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met
 695 700 705
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val
 710 715 720
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro
 725 730 735
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu
 740 745 750
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu
 755 760 765
 Gln Glu Gln Ala Asn Ser Thr
 770

<210> 340
 <211> 1572
 <212> DNA
 <213> Homo Sapien

<400> 340
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 cttttgaag ggtgtatgc ttgaaagcat tttctgtgct ttgatcacta 150
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
 catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250
 ggtatgagcgc atggagctca gtaagagctt tcgagttatac tgtatttatcc 300
 ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350
 accaaacact gtgaccaaagc agagttcttc agttctgaaa atgttaaagt 400

gtttgagtca attaatatgg acacaaatga catgtggta atgatgagaa 450
aagcttacaa atacgcctt gataagtata gagaccaata caactggttc 500
ttccttgcac gccccactac gtttgctatc attgaaaacc taaagtattt 550
tttgttaaaa aaggatccat cacagcctt ctatctaggc cacactataa 600
aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650
gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700
tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750
cagttgcct gaaatatgct ggagtattt cagaaaatgc agaagatgct 800
gatggaaaag atgtatTTAA taccaaATCT gttggcTTT ctattaaAGA 850
ggcaatgact tatCACCCCCC accaggtAGT agaaggctGT tgTTcAGATA 900
tggctgttac ttTAATGGA ctgactccaa atcagatgca tgtgatgatg 950
tatGGGGTAT accgcCTTAG ggcATTGGG catATTTCA atgatgcATT 1000
ggTTTCTTA CCTCCAAATG gttctgacAA tgactgagAA gtggtagAAA 1050
agcgtgaata tgatCTTGT ataggacGTg tgTTGTCATT atTTGTagTA 1100
gtAACTACAT atCCAATACA gctgtatGTT tCTTTTCTT ttctaatttG 1150
gtggcactgg tataaccaca cattaaAGTC agtagtACAT tttAAATGA 1200
gggtggTTT tttCTTTAAA acacatGAAC attgtAAATG tgTTGGAAAG 1250
aagtgtTTA agaATAATAA tttgCAAAT AAActATTAA taaATATTAT 1300
atgtgataAA ttCTAAATTA tgaACATTAG AAATCTGTGG ggcACATATT 1350
tttgctgatt ggtaaaaaaa tttaacagg tcttagcgt tctaagatAT 1400
gcaaATgata tctctAGTTG tgaATTGTG attAAAGTAA aactTTAGC 1450
tgtgtgtcc ctTACTTCT aataCTGATT tatgttctAA gcTCCCCAA 1500
gttccaatgg atttgCCTTC tcaAAATGTA caactaAGCA actAAAGAAA 1550
attAAAGTGA aagtTGAAAA at 1572

<210> 341
<211> 318
<212> PRT
<213> Homo Sapien

<400> 341

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	20							25					30	
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln
	35							40					45	
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
	50							55					60	
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
	65							70					75	
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
	80							85					90	
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
	95							100					105	
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
	110							115					120	
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
	125							130					135	
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
	140							145					150	
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
	155							160					165	
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr
	170							175					180	
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys
	185							190					195	
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln
	200							205					210	
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val
	215							220					225	
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala
	230							235					240	
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile
	245							250					255	
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys

260

265

270

Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln
275 280 285

Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly
290 295 300

His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser
305 310 315

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaagcc gttcttagacg cgg 23

<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

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<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 345
gggtgtgatg cttggaagca ttttctgtgc tttgatcact atgctaggac 50

<210> 346
<211> 25
<212> DNA
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<220>

<223> Synthetic Oligonucleotide Probe

<400> 346
ggatgcagg tggtgtctca tgggg 25

<210> 347
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347
ccctcatgta ccggctcc 18

<210> 348
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 348
ggattctaat acgactcact atagggtctca gaaaagcgca acagagaa 48

<210> 349
<211> 47
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 349
ctatgaaatt aaccctcact aaagggatgt cttccatgcc aaccttc 47

<210> 350
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 350
ggattctaat acgactcact atagggcgcc gatgtccact ggggctac 48

<210> 351
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 351
ctatgaaatt aaccctcact aaagggacga ggaagatggg cgatgg 48

<210> 352
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
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<400> 352
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<210> 353
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
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<400> 353
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<210> 354
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
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<400> 354
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<210> 355
<211> 48

SEARCHED
INDEXED
SERIALIZED
FILED

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 355
ctatgaaatt aaccctcact aaagggagct gccgatccca ctggatt 48

<210> 356
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
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<400> 356
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<210> 357
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 357
ctatgaaatt aaccctcact aaagggagcc cggcatggt ctcagtta 48

<210> 358
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 358
ggattctaat acgactcact atagggcgga aagatggcga ggaggag 47

<210> 359
<211> 48
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 359
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SEARCHED
INDEXED
SERIALIZED
FILED

<210> 360
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 360
ggattctaat acgactcact atagggctgt gcttcattc tgccagta 48

<210> 361
<211> 48
<212> DNA
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<400> 361
ctatgaaatt aaccctcact aaagggaggg tacaattaag gggtggat 48

<210> 362
<211> 47
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<400> 362
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<210> 363
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<210> 364
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<212> DNA
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<400> 364

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<210> 365
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<400> 365
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<400> 366
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<210> 367
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<212> DNA
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<400> 367
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<210> 368
<211> 47
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<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 368
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<210> 369
<211> 48
<212> DNA
<213> Artificial Sequence

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GENE BANK

<223> Synthetic Oligonucleotide Probe

<400> 369
ctatgaaatt aaccctcact aaaggaaag acatgtcatc gggagtgg 48

<210> 370
<211> 48
<212> DNA
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<220>

<223> Synthetic Oligonucleotide Probe

<400> 370
ggattctaat acgactcact atagggccgg gtggaggtgg aacagaaa 48

<210> 371
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 371
ctatgaaatt aaccctcact aaaggacac agacagagcc ccataacgc 48

<210> 372
<211> 47
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 372
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tgcttccttt cccaaatgtt ctatggact gttgctggga tccccatcct 200
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tcaatttattt tcggatttgtt gaaatggtag gaataaatcc tttgaacaaa 750

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 agagcaagaa catggccaca cccaccgccc cacacgagaa atttgcgc 850
 tgaacttcaa aggacttcat aagtatttgc tactctgata caaataaaaa 900
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 <212> PRT
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Ile Leu Phe Leu Ser Ala Cys Phe Ile Thr Arg Cys Val Val Thr
 35 40 45

Phe Arg Ile Phe Gln Thr Cys Asp Glu Lys Lys Phe Gln Leu Pro
 50 55 60

Glu Asn Phe Thr Glu Leu Ser Cys Tyr Asn Tyr Gly Ser Gly Ser
 65 70 75

Val Lys Asn Cys Cys Pro Leu Asn Trp Glu Tyr Phe Gln Ser Ser
 80 85 90

Cys Tyr Phe Phe Ser Thr Asp Thr Ile Ser Trp Ala Leu Ser Leu
 95 100 105

Lys Asn Cys Ser Ala Met Gly Ala His Leu Val Val Ile Asn Ser
 110 115 120

Gln Glu Glu Gln Glu Phe Leu Ser Tyr Lys Lys Pro Lys Met Arg
 125 130 135

Glu Phe Phe Ile Gly Leu Ser Asp Gln Val Val Glu Gly Gln Trp
 140 145 150

Gln Trp Val Asp Gly Thr Pro Leu Thr Lys Ser Leu Ser Phe Trp
 155 160 165

Asp Val Gly Glu Pro Asn Asn Ile Ala Thr Leu Glu Asp Cys Ala
 170 175 180

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val
185 190 195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile
200 205 210

Asn Pro Leu Asn Lys Gly Lys Ser Leu
215

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gcagatttg aggacagcca cctcca 26

<210> 382
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ggccttgcag acaaccgt 18

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<400> 385
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<400> 386

cacaaactcg aactgcttct g 21
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<400> 388
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<210> 389
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<400> 389
tgccagctgc atgctgccag tt 22

<210> 390
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<400> 390
cagaaggatg tcccgtggaa 20

<210> 391
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<400> 391
gcccgtgtcc actgcag 17

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atgtcctcca tgccccacgcg 20

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<400> 394
gagtgcgaca tcgagagctt 20

<210> 395
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<220>
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<400> 395
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<210> 396
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FOOTER SECTION

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<210> 397
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<400> 397
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<210> 398
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<400> 398
cctctggcgc ccccaactcaa 20

<210> 399
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<400> 399
ccaggagagc tggcgatg 18

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<400> 403
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<210> 408
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<210> 412
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<400> 412
agggttttat taagggccta cgct 24

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<400> 421
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<210> 422
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 35 40 45
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 50 55 60
 Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr
 65 70 75
 Thr Tyr Val Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly
 80 85 90
 Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val
 95 100 105
 Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg
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 Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val
 125 130 135
 Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val
 140 145 150
 Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly
 155 160 165
 His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu
 170 175 180
 Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe
 185 190 195

His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His
200 205 210

Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala
215 220 225

Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu
230 235 240

Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val
245 250 255

Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly
260 265 270

Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro
275 280 285

Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly
290 295 300

Asp Phe Arg His Lys Ser Ser Phe Val Ile
305 310